

### Human Nucleic Acid Sequences from Hysteromyomic Tissue

The invention relates to human nucleic acid sequences from hysteromyomic tissue, which code for gene products or portions thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death by cancer in women is hysteromyoma, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations.

They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

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A database that consists of so-called ESTs is used to look for candidate genes, i.e., genes that compared to the tumor tissue are more strongly expressed in normal tissue. ESTs (expressed sequence tags) are sequences of cDNAs, i.e., mRNAs transcribed in reverse, therefore molecules that reflect gene expression. The EST sequences are determined for normal and degenerated tissue. These databases are offered to some extent commercially by various companies. The ESTs of the LifeSeq database, which is used here, are generally between 150 and 350 nucleotides long. They represent a pattern that is unmistakable for a certain gene, although this gene is normally very much longer ( $> 2000$  nucleotides). By comparison of the expression patterns of normal and tumor tissue, ESTs can be identified that are important for tumor formation and proliferation. There is, however, the following problem: Since the EST sequences that are found can belong to different regions of an unknown gene due to different constructions of cDNA libraries, in this case a completely incorrect ratio of the occurrence of these ESTs in the respective tissue would arise. This would only be noticed when the complete gene is known and thus ESTs can be assigned to the same gene.

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It has now been found that this possibility of error can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, which play a role as candidate genes in the hysteryoma, have now been found.

Nucleic acid sequences Seq. ID Nos. 14-18, 30, 31 and 52 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a portion thereof, comprising

- a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 14-18, 30, 31 and 52.
- b) an allelic variation of the nucleic acid sequences named under a)
- or
- c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 14-18, 30, 31 or a complementary or allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

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The invention also relates to nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52, which are expressed elevated in the hystero myoma.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 14-18, 30, 31 and 52.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 14-18, 30, 31 and 52 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

A large number of expression cassettes or vectors and promoters which can be used are known in the literature.

Expression cassettes or vectors are defined as:

1. bacterial, such as, e.g., phagescript, pBs,  $\phi$ X174, pBluescript SK, pBs KS, pNH8a, pNH16a, pNH18a, pNH46a (Stratagene), pTrc99A, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia),
2. eukaryotic, such as, e.g., pWLneo, pSV2cat, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia).

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Control or regulatory sequences are defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The DNA sequences located on the expression cassette can code a fusion protein which comprises a known protein and a bioactive polypeptide fragment.

The expression cassettes are likewise the subject matter of this invention.

The nucleic acid fragments according to the invention can be used to produce full-length genes. The genes that can be obtained are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

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The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

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The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides, according to the sequence protocols ORF ID Nos. 32-51 and ORF ID Nos. 53-55.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of ORF ID Nos. 32-51 and ORF ID Nos. 53-55 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by the nucleic acids of sequences Seq. ID Nos. 1-31 and Seq. ID No. 52 according to the invention.

Antibodies are defined especially as monoclonal antibodies.

The antibodies according to the invention can be identified by, i.a., a phage display process. These antibodies are also the subject matter of the invention.

The polypeptide partial sequences according to the invention can be used in a phage display process. The polypeptides that are identified with this process and that bind to the polypeptide

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partial sequences according to the invention are also the subject matter of the invention.

The nucleic acid sequences according to the invention can also be used in a phage display process.

The polypeptides of sequences Seq. ID Nos. 32-51 and Seq. ID Nos. 53-55 according to the invention can also be used as tools for finding active ingredients against hystero myoma, which is likewise the subject matter of this invention.

Likewise the subject matter of this invention is the use of nucleic acid sequences according to sequences Seq. ID No. 1 to Seq. ID No. 31 and Seq. ID 52 for expression of polypeptides, which can be used as tools for finding active ingredients against hystero myoma.

The invention also relates to the use of the found polypeptide partial sequences Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55 as pharmaceutical agents in the gene therapy for treatment of hystero myoma or for the production of a pharmaceutical agent for treatment of hystero myoma.

The invention also relates to pharmaceutical agents that contain at least one polypeptide partial sequence Seq. ID Nos. 32 to 51 and Seq. ID Nos. 53-55.

The nucleic acid sequences found according to the invention can also be genomic or mRNA sequences.

The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID Nos. 1-31, and 52, and their use

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together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences) Seq. ID Nos. 1-31 and 52, genomic BAC, PAC and cosmid libraries are screened, and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes, and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-31 and 52, for use as vehicles for gene transfer.

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## Meanings of Technical Terms and Abbreviations

Nucleic acids= Nucleic acids in this invention are defined as:

mRNA, partial cDNA, full-length cDNA and genomic genes (chromosomes)

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence

Contig = A set of DNA sequences that can be combined as a result of very great similarities into one sequence (consensus)

Singleton = A contig that contains only one sequence

Module = Domain of a protein with a defined sequence, which represents one structural unit and which occurs in various proteins

N = selectively the nucleotide A, T, G or C

X = selectively one of the 20 naturally occurring amino acids

## Explanation of the Alignment Parameters

minimal initial match = minimal initial identity area

maximum pads per read = maximum number of insertions

~~maximum percent mismatch = maximum deviation in %~~

## Explanation of Figures

Figure 1 shows the systematic gene search in the Incyte LifeSeq database

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

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- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

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The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

#### **Example 1**

##### **Search for Tumor-related Candidate Genes**

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

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Figures 2b1-2b4 illustrate the lengthening of the hysteryomyomic tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another.)

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

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**Example 2****Algorithm for Identification and Lengthening of Partial cDNA Sequences with Altered Expression Pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

**2.1. Electronic Northern Blot**

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

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**2.1.1**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 30 was found, which occurs more frequently in the hystero myomic tissue than in normal tissue.

The result is as follows:

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Electronic Northern for SEQ. ID NO.: 30

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0010	0.0000	undef	0.0000
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0021	5.1181	0.1954
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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**2.1.2.**

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 31 was found, which occurs more frequently in the hysteryomic tissue than in normal tissue.

The result is as follows:

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Electronic Northern for SEQ. ID NO.: 31

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0102	0.4064	2.4605
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0224	0.0000	undef	undef
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0061			
White blood cells	0.0213			
Cervix				

FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Development	Breast 0.0000
Gastrointestinal 0.0000	Ovary_n 0.0000
Brain 0.0028	Ovary_t 0.0000
Hematopoietic 0.0125	Endocrine tissue 0.0000
Skin 0.0000	Fetal 0.0000
Hepatic 0.0000	Gastrointestinal 0.0000
Heart-blood vessels 0.0000	Hematopoietic 0.0000
Lung 0.0036	Skin-muscle 0.0000
Suprarenal gland 0.0036	Testicles 0.0000
Kidney 0.0254	Lung 0.0082
Placenta 0.0062	Nerves 0.0000
Prostate 0.0303	Prostate 0.0000
Sensory organs 0.0000	Sensory Organs 0.0000
	Uterus_n 0.0000
0.0126	

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In an analogous procedure, the following Northernblots were also found:

Electronic Northern for SEQ. ID NO.: 1

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0468	0.0562	0.8321	1.2018
Breast	0.0576	0.0752	0.7656	1.3062
Small intestine	0.0766	0.0662	1.1586	0.8631
Ovary	0.0509	0.0650	0.7829	1.2774
Endocrine tissue	0.0596	0.0702	0.8491	1.1778
Gastrointestinal	0.0690	0.1203	0.5735	1.7438
Brain	0.0850	0.0873	0.9741	1.0266
Hematopoietic	0.0722	0.0379	1.9056	0.5248
Skin	0.0918	0.0000	undef	0.0000
Hepatic	0.0143	0.1100	0.1298	7.7066
Heart	0.1123	0.0275	4.0862	0.2447
Testicles	0.0518	0.0819	0.6325	1.5809
Lung	0.1080	0.0879	1.2287	0.8138
Stomach-esophagus	0.0676	0.0307	2.2059	0.4533
Muscle-skeleton	0.0737	0.0780	0.9445	1.0587
Kidney	0.0407	0.0890	0.4575	2.1857
Pancreas	0.0463	0.0552	0.8376	1.1939
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0436	0.0554	0.7874	1.2700
Uterus-endometrium	0.0338	0.0000	undef	0.0000
Uterus-myometrium	0.0534	0.1426	0.3741	2.6732
Uterus-general	0.0255	0.0000	undef	0.0000
Breast hyperplasia	0.0863			
Prostate hyperplasia	0.0535			
Seminal vesicle	0.0890			
Sensory organs	0.0588			
White blood cells	0.0772			
Cervix	0.1171			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0204
Gastrointestinal	0.0583	Ovary_n	0.1595
Brain	0.0500	Ovary_t	0.0051
Hematopoietic	0.0590	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0256
Hepatic	0.0000	Gastrointestinal	0.0488
Heart-blood vessels	0.0462	Hematopoietic	0.0000
Lung	0.0578	Skin-muscle	0.0227
Suprarenal gland	0.0254	Testicles	0.0154
Kidney	0.0679	Lung	0.0082
Placenta	0.0545	Nerves	0.0191
Prostate	0.2493	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 2

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0039	0.0102	0.3814	2.6222
Small intestine	0.0128	0.0038	3.4026	0.2939
Ovary	0.0031	0.0165	0.1854	5.3946
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0017	0.0075	0.2264	4.4166
Brain	0.0019	0.0093	0.2071	4.8289
Hematopoietic	0.0022	0.0103	0.2160	4.6299
Skin	0.0040	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0065	0.0000	undef
Testicles	0.0011	0.0137	0.0771	12.9706
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0021	0.0082	0.2540	3.9367
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0120	0.0000	undef
Pancreas	0.0054	0.0000	undef	0.0000
Penis	0.0000	0.0055	0.0000	undef
Prostate	0.0030	0.0000	undef	0.0000
Uterus-endometrium	0.0000	0.0021	0.0000	undef
Uterus-myometrium	0.0000	0.0528	0.0000	undef
Uterus-general	0.0051	0.0408	0.0000	undef
Breast hyperplasia	0.0064	0.0954	0.0534	18.7357
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0009			
Cervix	0.0000			

FETUS		STANDARDIZED/SUBTRACTED	
	% frequency	LIBRARIES	
		% frequency	
Development		Breast	0.0000
Gastrointestinal	0.0974	Ovary_n	0.0000
Brain	0.0333	Ovary_t	0.0000
Hematopoietic	0.0063	Endocrine tissue	0.0000
Skin	0.0157	Fetal	0.0384
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0249		0.0259
Suprarenal gland	0.0325	Skin-muscle	0.0000
Kidney	0.0761	Testicles	0.0328
Placenta	0.0618	Lung	0.0171
Prostate	0.0727	Nerves	0.0137
Sensory organs	0.0249	Prostate	0.0000
	0.0000	Sensory Organs	0.0083
		Uterus n	

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Electronic Northern for SEQ. ID NO.: 3

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.1103	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0140	0.0010	13.6792	0.0731
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0815	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0030			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0090
Prostate	0.0000	Prostate	0.0137
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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Electronic Northern for SEQ. ID NO.: 4

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0077	1.0170	0.9833
Breast	0.0026	0.0038	0.6805	1.4694
Small intestine	0.0031	0.0165	0.1854	5.3946
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0046	0.0000	undef
Brain	0.0007	0.0031	0.2400	4.1669
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.1695	0.0000	undef
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0095	0.0412	0.2313	4.3235
Testicles	0.0000	0.0000	undef	undef
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0017	0.0120	0.1428	7.0040
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0033	0.0055	0.5983	1.6714
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0021	0.0000	undef
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0883	0.1727	5.7919
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0032			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0278	Ovary_n	0.0068
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0213	Skin-muscle	0.0130
Suprarenal gland	0.0253	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0185	Nerves	0.0000
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0000

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## Electronic Northern for SEQ. ID NO.: 5

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0390	0.0332	1.1734	0.8522
Small intestine	0.0345	0.0414	0.8352	1.1973
Ovary	0.0399	0.0662	0.6024	1.6599
Endocrine tissue	0.0359	0.0546	0.6579	1.5201
Gastrointestinal	0.0528	0.0351	1.5040	0.6649
Brain	0.0172	0.0185	0.9319	1.0731
Hematopoietic	0.0214	0.0359	0.5965	1.6763
Skin	0.0294	0.0379	0.7763	1.2881
Hepatic	0.0257	0.1695	0.1516	6.5954
Heart	0.0476	0.0323	1.4706	0.6800
Testicles	0.0276	0.0000	undef	0.0000
Lung	0.0633	0.0234	2.7059	0.3696
Stomach-esophagus	0.0312	0.0266	1.1724	0.8530
Muscle-skeleton	0.0387	0.0153	2.5211	0.3967
Kidney	0.0308	0.0360	0.8567	1.1673
Pancreas	0.0326	0.0548	0.5948	1.6813
Penis	0.0132	0.0221	0.5983	1.6714
Prostate	0.0479	0.0000	undef	0.0000
Uterus-endometrium	0.0153	0.0319	0.4777	2.0934
Uterus-myometrium	0.0473	0.0528	0.8962	1.1158
Uterus-general	0.0305	0.1019	0.2993	3.3415
Breast hyperplasia	0.0560	0.1908	0.2936	3.4065
Prostate hyperplasia	0.0448			
Seminal vesicle	0.0446			
Sensory organs	0.1513			
White blood cells	0.0235			
Cervix	0.0061			
	0.0426			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal	0.0974	Ovary_n	0.0000
Brain	0.0222	Ovary_t	0.0051
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0197	Fetal	0.0099
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0356	Skin-muscle	0.0324
Suprarenal gland	0.0325	Testicles	0.0231
Kidney	0.0000	Lung	0.0328
Placenta	0.0185	Nerves	0.0131
Prostate	0.0909	Prostate	0.0068
Sensory organs	0.1496	Sensory Organs	0.0077
	0.0126	Uterus_n	0.0208

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## Electronic Northern for SEQ. ID NO.: 6

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0429	0.1278	0.3356	2.9798
Breast	0.1036	0.1203	0.8613	1.1610
Small intestine	0.0215	0.0992	0.2163	4.6240
Ovary	0.0599	0.0702	0.8528	1.1726
Endocrine tissue	0.0783	0.0426	1.8380	0.5441
Gastrointestinal	0.0249	0.0786	0.3167	3.1574
Brain	0.0429	0.1284	0.3341	2.9935
Hematopoietic	0.0227	0.1136	0.2000	5.0008
Skin	0.0844	0.1695	0.4982	2.0073
Hepatic	0.0523	0.0712	0.7353	1.3600
Heart	0.0922	0.1649	0.5590	1.7890
Testicles	0.0460	0.0585	0.7872	1.2704
Lung	0.0447	0.0797	0.5601	1.7853
Stomach-esophagus	0.0000	0.0537	0.0000	undef
Muscle-skeleton	0.1490	0.1380	1.0801	0.9258
Kidney	0.0489	0.0479	1.0196	0.9808
Pancreas	0.0149	0.1049	0.1417	7.0571
Penis	0.0509	0.1333	0.3819	2.6187
Prostate	0.0196	0.0319	0.6142	1.6282
Uterus-endometrium	0.0676	0.1583	0.4268	2.3432
Uterus-myometrium	0.0381	0.3260	0.1169	8.5541
Uterus-general	0.0560	0.0000	undef	0.0000
Breast hyperplasia	0.0863			
Prostate hyperplasia	0.0297			
Seminal vesicle	0.0089			
Sensory organs	0.0353			
White blood cells	0.0078			
Cervix	0.0213			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.1670	Ovary_n	0.0476
Brain	0.1444	Ovary_t	0.1595
Hematopoietic	0.0125	Endocrine tissue	0.0203
Skin	0.0629	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0379
Heart-blood vessels	0.0122	Hematopoietic	0.0122
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0889	Testicles	0.0486
Kidney	0.0759	Lung	0.0077
Placenta	0.2535	Nerves	0.0164
Prostate	0.1112	Prostate	0.0251
Sensory organs	0.1091	Sensory Organs	0.0068
	0.1247	Uterus_n	0.0155
	0.1004		0.0167

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Electronic Northern for SEQ. ID NO.: 7

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0117	0.0051	2.2882	0.4370
Breast	0.0128	0.0075	1.7013	0.5878
Small intestine	0.0153	0.0331	0.4634	2.1579
Ovary	0.0150	0.0104	1.4391	0.6949
Endocrine tissue	0.0085	0.0050	1.6981	0.5889
Gastrointestinal	0.0096	0.0278	0.3451	2.8974
Brain	0.0059	0.0113	0.5236	1.9098
Hematopoietic	0.0254	0.0000	undef	0.0000
Skin	0.0257	0.0000	undef	0.0000
Hepatic	0.0143	0.0194	0.7353	1.3600
Heart	0.0106	0.0000	undef	0.0000
Testicles	0.0058	0.0234	0.2460	4.0652
Lung	0.0104	0.0245	0.4234	2.3620
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0051	0.0360	0.1428	7.0040
Kidney	0.0244	0.0068	3.5687	0.2802
Pancreas	0.0083	0.0000	undef	0.0000
Penis	0.0180	0.0000	undef	0.0000
Prostate	0.0218	0.0064	3.4121	0.2931
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0408	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0235			
White blood cells	0.0208			
Cervix	0.0213			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0083	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0101
Skin	0.0000	Fetal	0.0245
Hepatic	0.0000	Gastrointestinal	0.0093
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0071	Skin-muscle	0.0342
Suprarenal gland	0.0036	Testicles	0.0097
Kidney	0.0000	Lung	0.0154
Placenta	0.0309	Nerves	0.0082
Prostate	0.0061	Prostate	0.0080
Sensory organs	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000
			0.0042

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Electronic Northern for SEQ. ID NO.: 8

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0312	0.0460	0.6780	1.4750
Breast	0.0192	0.0282	0.6805	1.4694
Small intestine	0.0368	0.0000	undef	0.0000
Ovary	0.0210	0.0364	0.5756	1.7372
Endocrine tissue	0.0290	0.0326	0.8882	1.1258
Gastrointestinal	0.0460	0.0231	1.9880	0.5030
Brain	0.0532	0.0585	0.9094	1.0996
Hematopoietic	0.0361	0.0379	0.9528	1.0496
Skin	0.0367	0.0000	undef	0.0000
Hepatic	0.0048	0.0647	0.0735	13.5999
Heart	0.0699	0.0412	1.6961	0.5896
Testicles	0.0288	0.4210	0.0683	14.6349
Lung	0.0343	0.0368	0.9314	1.0737
Stomach-esophagus	0.0773	0.0230	3.3614	0.2975
Muscle-skeleton	0.0497	0.0660	0.7528	1.3283
Kidney	0.0353	0.1575	0.2241	4.4619
Pancreas	0.0165	0.0939	0.1760	5.6828
Penis	0.0299	0.0267	1.1232	0.8903
Prostate	0.0196	0.0298	0.6580	1.5197
Uterus-endometrium	0.0270	0.1583	0.1707	5.8579
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0954	0.0534	18.7357
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0505			
Seminal vesicle	0.0890			
Sensory organs	0.0353			
White blood cells	0.0399			
Cervix	0.0319			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0417	Ovary_n	0.0000
Brain	0.0333	Ovary_t	0.0152
Hematopoietic	0.0313	Endocrine tissue	0.0000
Skin	0.0197	Fetal	0.0082
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0783	Skin-muscle	0.0032
Suprarenal gland	0.0217	Testicles	0.0077
Kidney	0.0507	Lung	0.0082
Placenta	0.0309	Nerves	0.0141
Prostate	0.0727	Prostate	0.0000
Sensory organs	0.0997	Sensory Organs	0.0310
	0.0000	Uterus_n	0.0125

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Electronic Northern for SEQ. ID NO.: 9

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0468	0.0204	2.2882	0.4370
Breast	0.0205	0.0451	0.4537	2.2042
Small intestine	0.0307	0.0331	0.9268	1.0789
Ovary	0.0539	0.0468	1.1513	0.8686
Endocrine tissue	0.0562	0.0527	1.0674	0.9369
Gastrointestinal	0.0249	0.0324	0.7692	1.3001
Brain	0.0333	0.0318	1.0451	0.9568
Hematopoietic	0.0388	0.0379	1.0234	0.9772
Skin	0.0257	0.1695	0.1516	6.5954
Hepatic	0.0095	0.0259	0.3676	2.7200
Heart	0.0540	0.0000	undef	0.0000
Testicles	0.0173	0.0702	0.2460	4.0652
Lung	0.0291	0.0491	0.5927	1.6872
Stomach-esophagus	0.0000	0.0230	0.0000	undef
Muscle-skeleton	0.0206	0.1140	0.1803	5.5448
Kidney	0.0733	0.0274	2.6765	0.3736
Pancreas	0.0264	0.0331	0.7977	1.2536
Penis	0.0269	0.0533	0.5054	1.9786
Prostate	0.0501	0.0341	1.4715	0.6796
Uterus-endometrium	0.0541	0.2639	0.2049	4.8816
Uterus-myometrium	0.0152	0.0611	0.2494	4.0097
Uterus-general	0.0204	0.0000	undef	0.0000
Breast hyperplasia	0.0512			
Prostate hyperplasia	0.0386			
Seminal vesicle	0.0623			
Sensory organs	0.0470			
White blood cells	0.0286			
Cervix	0.0426			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0068
Gastrointestinal	0.0557	Ovary_n	0.1595
Brain	0.0666	Ovary_t	0.0051
Hematopoietic	0.0626	Endocrine tissue	0.0245
Skin	0.0786	Fetal	0.0256
Hepatic	0.0000	Gastrointestinal	0.0732
Heart-blood vessels	0.0260	Hematopoietic	0.0057
Lung	0.0818	Skin-muscle	0.0551
Suprarenal gland	0.0867	Testicles	0.0309
Kidney	0.0761	Lung	0.0737
Placenta	0.0432	Nerves	0.0231
Prostate	0.0606	Prostate	0.0137
Sensory organs	0.0249	Sensory Organs	0.0310
	0.0628	Uterus_n	0.0333

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## Electronic Northern for SEQ. ID NO.: 10

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.1131	0.1431	0.7900	1.2659
Breast	0.1356	0.1692	0.8015	1.2476
Small intestine	0.1962	0.0165	11.8636	0.0843
Ovary	0.1827	0.2446	0.7471	1.3385
Endocrine tissue	0.1090	0.1329	0.8202	1.2192
Gastrointestinal	0.1878	0.2590	0.7248	1.3797
Brain	0.1035	0.1325	0.7814	1.2798
Hematopoietic	0.2700	0.1894	1.4257	0.7014
Skin	0.1358	0.0847	1.6028	0.6239
Hepatic	0.0428	0.1812	0.2363	4.2311
Heart	0.2586	0.0137	18.8118	0.0532
Testicles	0.0633	0.1403	0.4510	2.2174
Lung	0.3231	0.2229	1.4495	0.6899
Stomach-esophagus	0.1643	0.2147	0.7653	1.3066
Muscle-skeleton	0.1970	0.0960	2.0524	0.4872
Kidney	0.1222	0.2328	0.5248	1.9055
Pancreas	0.0876	0.1767	0.4955	2.0183
Penis	0.1407	0.1600	0.8798	1.1366
Prostate	0.1003	0.0766	1.3080	0.7645
Uterus-endometrium	0.1824	0.0528	3.4569	0.2893
Uterus-myometrium	0.1677	0.3804	0.4409	2.2681
Uterus-general	0.2292	0.0000	undef	0.0000
Breast hyperplasia	0.0735			
Prostate hyperplasia	0.0684			
Seminal vesicle	0.1335			
Sensory organs	0.0470			
White blood cells	0.2749			
Cervix	0.0958			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal	0.0139	Ovary_n	0.3190
Brain	0.0639	Ovary_t	0.0709
Hematopoietic	0.1063	Endocrine tissue	0.0000
Skin	0.1258	Fetal	0.0326
Hepatic	0.2513	Gastrointestinal	0.1464
Heart-blood vessels	0.0260	Hematopoietic	0.0000
Lung	0.0712	Skin-muscle	0.1328
Suprarenal gland	0.1517	Testicles	0.0154
Kidney	0.0000	Lung	0.2211
Placenta	0.0988	Nerves	0.0311
Prostate	0.0909	Prostate	0.0410
Sensory organs	0.1745	Sensory Organs	0.0000
	0.0377	Uterus_n	0.0333

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Electronic Northern for SEQ. ID NO.: 11

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0156	0.0051	3.0509	0.3278
Small intestine	0.0064	0.0113	0.5671	1.7633
Ovary	0.0031	0.0000	undef	0.0000
Endocrine tissue	0.0240	0.0234	1.0233	0.9772
Gastrointestinal	0.0068	0.0100	0.6792	1.4722
Brain	0.0096	0.0046	2.0708	0.4829
Hematopoietic	0.0022	0.0257	0.0864	11.5747
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0110	0.0000	undef	0.0000
Heart	0.0238	0.0065	3.6765	0.2720
Testicles	0.0276	0.0275	1.0023	0.9977
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0083	0.0245	0.3387	2.9526
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0086	0.0060	1.4278	0.7004
Pancreas	0.0081	0.0616	0.1322	7.5658
Penis	0.0165	0.0000	undef	0.0000
Prostate	0.0120	0.0267	0.4493	2.2259
Uterus-endometrium	0.0065	0.0085	0.7677	1.3026
Uterus-myometrium	0.0270	0.0000	undef	0.0000
Uterus-general	0.0076	0.0951	0.0802	12.4748
Breast hyperplasia	0.0968	0.0000	undef	0.0000
Prostate hyperplasia	0.0096			
Seminal vesicle	0.0089			
Sensory organs	0.0089			
White blood cells	0.0706			
Cervix	0.0000			
	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0139	Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0708	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0233
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0320	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0648
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0124	Lung	0.0164
Placenta	0.2121	Nerves	0.0010
Prostate	0.0000	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0083

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Electronic Northern for SEQ. ID NO.: 12

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0351	0.3093	0.1135	8.8135
Breast	0.0269	0.0470	0.5716	1.7493
Small intestine	0.0092	0.0662	0.1390	7.1929
Ovary	0.0569	0.0182	3.1248	0.3200
Endocrine tissue	0.0528	0.0502	1.0528	0.9498
Gastrointestinal	0.0019	0.0093	0.2071	4.8289
Brain	0.0022	0.0873	0.0254	39.3541
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0220	0.5085	0.0433	23.0839
Hepatic	0.0285	0.0582	0.4902	2.0400
Heart	0.0191	0.0000	undef	0.0000
Testicles	0.0115	0.0000	undef	0.0000
Lung	0.0114	0.0061	1.8628	0.5368
Stomach-esophagus	0.0193	0.0077	2.5211	0.3967
Muscle-skeleton	0.0771	0.0540	1.4278	0.7004
Kidney	0.0489	0.0137	3.5687	0.2802
Pancreas	0.0264	0.0442	0.5983	1.6714
Penis	0.0090	0.1066	0.0842	11.8713
Prostate	0.0000	0.0064	0.0000	undef
Uterus-endometrium	0.0743	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.1494	0.2551	3.9206
Uterus-general	0.0153	0.0954	0.1601	6.2452
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0059			
Seminal vesicle	0.0000			
Sensory organs	0.0118			
White blood cells	0.0000			
Cervix	0.0000			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0612
Gastrointestinal	0.0696	Ovary_n	0.0000
Brain	0.4387	Ovary_t	0.1114
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.2713	Fetal	0.4665
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	1.6121	Hematopoietic	0.0000
Lung	0.0605	Skin-muscle	0.0000
Suprarenal gland	0.1770	Testicles	0.0000
Kidney	1.1663	Lung	0.0000
Placenta	0.8092	Nerves	0.0030
Prostate	0.7635	Prostate	0.0068
Sensory organs	0.0499	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0291

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Electronic Northern for SEQ. ID NO.: 13

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder				
Breast	0.0078	0.0204	0.3814	2.6222
Small intestine	0.0256	0.0432	0.5918	1.6899
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0060	0.0078	0.7675	1.3029
Gastrointestinal	0.0000	0.0050	0.0000	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0074	0.0216	0.3428	2.9168
Skin	0.0013	0.0000	undef	0.0000
Hepatic	0.0073	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0021	0.0000	undef	0.0000
Lung	0.0115	0.0468	0.2460	4.0652
Stomach-esophagus	0.0031	0.0082	0.3810	2.6245
Muscle-skeleton	0.0580	0.0000	undef	0.0000
Kidney	0.0000	0.0300	0.0000	undef
Pancreas	0.0027	0.0000	undef	0.0000
Penis	0.0033	0.0276	0.1197	8.3571
Prostate	0.0210	0.1066	0.1966	5.0877
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0135	0.0000	undef	0.0000
Uterus-general	0.0305	0.0883	0.3453	2.8959
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0160			
Seminal vesicle	0.0059			
Sensory organs	0.0356			
White blood cells	0.0000			
Cervix	0.0035			
	0.0639			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0408
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.1266
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0047
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0032
Suprarenal gland	0.0145	Testicles	0.0000
Kidney	0.0761	Lung	0.0000
Placenta	0.0247	Nerves	0.0030
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0208

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Electronic Northern for SEQ. ID NO.: 14

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0195	0.0051	3.8136	0.2622
Small intestine	0.0051	0.0132	0.3889	2.5715
Ovary	0.0061	0.0000	undef	0.0000
Endocrine tissue	0.0150	0.0130	1.1513	0.8686
Gastrointestinal	0.0153	0.0150	1.0189	0.9815
Brain	0.0115	0.0000	undef	0.0000
Hematopoietic	0.0133	0.0133	0.9969	1.0031
Skin	0.0174	0.0000	undef	0.0000
Hepatic	0.0147	0.0000	undef	0.0000
Heart	0.0000	0.0194	0.0000	undef
Testicles	0.0265	0.0000	undef	0.0000
Lung	0.0058	0.0000	undef	0.0000
Stomach-esophagus	0.0042	0.0164	0.2540	3.9367
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0069	0.0540	0.1269	7.8795
Pancreas	0.0217	0.0274	0.7930	1.2610
Penis	0.0165	0.0055	2.9915	0.3343
Prostate	0.0090	0.0000	undef	0.0000
Uterus-endometrium	0.0087	0.0170	0.5118	1.9538
Uterus-myometrium	0.0338	0.2111	0.1600	6.2484
Uterus-general	0.0076	0.0475	0.1603	6.2374
Breast hyperplasia	0.0000	0.0000	undef	undef
Prostate hyperplasia	0.0320			
Seminal vesicle	0.0238			
Sensory organs	0.0267			
White blood cells	0.0000			
Cervix	0.0069			
	0.0213			

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FETUS		STANDARDIZED/SUBTRACTED	
% frequency		LIBRARIES	
		% frequency	
Development		Breast	
Gastrointestinal	0.0417	Ovary_n	0.0068
Brain	0.0139	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0051
Skin	0.0157	Fetal	0.0245
Hepatic	0.0000	Gastrointestinal	0.0035
Heart-blood vessels	0.0000	Hematopoietic	0.0244
Lung	0.0427	Skin-muscle	0.0000
Suprarenal gland	0.0253	Testicles	0.0065
Kidney	0.0000	Lung	0.0000
Placenta	0.0124	Nerves	0.0082
Prostate	0.0121	Prostate	0.0050
Sensory organs	0.0000	Sensory Organs	0.0137
	0.0126	Uterus_n	0.0155
			0.0042

Electronic Northern for SEQ. ID NO.: 15

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0078	0.0102	0.7627	1.3111
Breast	0.0026	0.0150	0.1701	5.8778
Small intestine	0.0184	0.0496	0.3707	2.6973
Ovary	0.0000	0.0052	0.0000	undef
Endocrine tissue	0.0000	0.0025	0.0000	undef
Gastrointestinal	0.0000	0.0093	0.0000	undef
Brain	0.0007	0.0072	0.1029	9.7228
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0021	0.0041	0.5080	1.9684
Stomach-esophagus	0.0000	0.0307	0.0000	undef
Muscle-skeleton	0.0086	0.0240	0.3569	2.8016
Kidney	0.0027	0.0000	undef	0.0000
Pancreas	0.0000	0.0055	0.0000	undef
Penis	0.0240	0.0000	undef	0.0000
Prostate	0.0065	0.0021	3.0709	0.3256
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0096			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0000	Lung	0.0020
Placenta	0.0000	Nerves	0.0000
Prostate	0.0249	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

002221-00437960



## Electronic Northern for SEQ. ID NO.: 16

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0039	0.0153	0.2542	3.9333
Breast	0.0077	0.0038	2.0416	0.4898
Small intestine	0.0123	0.0000	undef	0.0000
Ovary	0.0060	0.0026	2.3025	0.4343
Endocrine tissue	0.0119	0.0251	0.4755	2.1032
Gastrointestinal	0.0096	0.0139	0.6903	1.4487
Brain	0.0163	0.0246	0.6600	1.5152
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0095	0.0065	1.4706	0.6800
Heart	0.0180	0.0000	undef	0.0000
Testicles	0.0000	0.0117	0.0000	undef
Lung	0.0135	0.0082	1.6511	0.6057
Stomach-esophagus	0.0000	0.0153	0.0000	undef
Muscle-skeleton	0.0069	0.0060	1.1422	0.8755
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0033	0.0276	0.1197	8.3571
Penis	0.0090	0.0267	0.3369	2.9678
Prostate	0.0196	0.0128	1.5354	0.6513
Uterus-endometrium	0.0068	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0408	0.0000	undef
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0128			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0267			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0375	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0012
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0071	Skin-muscle	0.0097
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0507	Lung	0.0082
Placenta	0.0124	Nerves	0.0050
Prostate	0.0061	Prostate	0.0000
Sensory organs	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0083

00673400-122700

Electronic Northern for SEQ. ID NO.: 17

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0307	0.0338	0.9074	1.1021
Small intestine	0.0184	0.0165	1.1122	0.8991
Ovary	0.0509	0.0286	1.7792	0.5620
Endocrine tissue	0.0375	0.0301	1.2453	0.8030
Gastrointestinal	0.0153	0.0093	1.6567	0.6036
Brain	0.0222	0.0452	0.4909	2.0372
Hematopoietic	0.0160	0.0000	undef	0.0000
Skin	0.0661	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.6266
Heart	0.0636	0.0000	undef	0.0000
Testicles	0.0173	0.0117	1.4759	0.6775
Lung	0.0177	0.0532	0.3322	3.0104
Stomach-esophagus	0.0483	0.0000	undef	0.0000
Muscle-skeleton	0.0137	0.0960	0.1428	7.0040
Kidney	0.0217	0.0685	0.3172	3.1524
Pancreas	0.0264	0.0055	4.7864	0.2089
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0283	0.0341	0.8317	1.2024
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0671			
Prostate hyperplasia	0.0476			
Seminal vesicle	0.0356			
Sensory organs	0.0353			
White blood cells	0.0121			
Cervix	0.0532			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.0557	Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0688	Ovary_t	0.0203
Hematopoietic	0.0275	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0169
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0534	Hematopoietic	0.0000
Lung	0.0831	Skin-muscle	0.0259
Suprarenal gland	0.1014	Testicles	0.0000
Kidney	0.0741	Lung	0.0082
Placenta	0.0182	Nerves	0.0050
Prostate	0.1247	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	0.0167

002221-004E2960

Electronic Northern for SEQ. ID NO.: 18

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0195	0.0179	1.0896	0.9178
Breast	0.0371	0.0357	1.0387	0.9627
Small intestine	0.0245	0.0331	0.7415	1.3487
Ovary	0.0479	0.0390	1.2280	0.8143
Endocrine tissue	0.0358	0.0326	1.0972	0.9114
Gastrointestinal	0.0153	0.0093	1.6567	0.6036
Brain	0.0229	0.0524	0.4376	2.2851
Hematopoietic	0.0147	0.0000	undef	0.0000
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0143	0.0518	0.2757	3.6266
Heart	0.0593	0.0000	undef	0.0000
Testicles	0.0115	0.0117	0.9839	1.0163
Lung	0.0145	0.0491	0.2964	3.3743
Stomach-esophagus	0.0290	0.0000	undef	0.0000
Muscle-skeleton	0.0120	0.1140	0.1052	9.5055
Kidney	0.0299	0.0616	0.4846	2.0634
Pancreas	0.0281	0.0055	5.0855	0.1966
Penis	0.0449	0.0000	undef	0.0000
Prostate	0.0349	0.0319	1.0919	0.9159
Uterus-endometrium	0.0203	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0679	0.2245	4.4553
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0446			
Seminal vesicle	0.0356			
Sensory organs	0.0235			
White blood cells	0.0130			
Cervix	0.0532			

STANDARDIZED/SUBTRACTED  
LIBRARIES

	FETUS % frequency		% frequency
Development		Breast	0.0000
Gastrointestinal	0.0417	Ovary_n	0.0000
Brain	0.0333	Ovary_t	0.0253
Hematopoietic	0.0688	Endocrine tissue	0.0245
Skin	0.0275	Fetal	0.0326
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0427	Skin-muscle	0.0518
Suprarenal gland	0.0867	Testicles	0.0000
Kidney	0.1268	Lung	0.0082
Placenta	0.0741	Nerves	0.0090
Prostate	0.0182	Prostate	0.0137
Sensory organs	0.1247	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0208

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Electronic Northern for SEQ. ID NO.: 19

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0351	0.0332	1.0561	0.9469
Small intestine	0.0269	0.0376	0.7146	1.3995
Ovary	0.0337	0.0992	0.3398	2.9425
Endocrine tissue	0.0240	0.0312	0.7675	1.3029
Gastrointestinal	0.0409	0.0075	5.4340	0.1840
Brain	0.0268	0.0971	0.2761	3.6217
Hematopoietic	0.0059	0.0113	0.5236	1.9098
Skin	0.0013	0.2273	0.0059	170.0273
Hepatic	0.0330	0.0000	undef	0.0000
Heart	0.0095	0.0388	0.2451	4.0800
Testicles	0.0223	0.0000	undef	0.0000
Lung	0.0173	0.0351	0.4920	2.0326
Stomach-esophagus	0.0395	0.0900	0.4388	2.2792
Muscle-skeleton	0.0000	0.0077	0.0000	undef
Kidney	0.0857	0.1920	0.4462	2.2413
Pancreas	0.0136	0.0205	0.6609	1.5132
Penis	0.0198	0.0221	0.8974	1.1143
Prostate	0.0629	0.0800	0.7862	1.2719
Uterus-endometrium	0.0087	0.0106	0.8189	1.2211
Uterus-myometrium	0.0676	0.0000	undef	0.0000
Uterus-general	0.0686	0.1630	0.4208	2.3761
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0735			
Seminal vesicle	0.0416			
Sensory organs	0.0000			
White blood cells	0.0235			
Cervix	0.0000			
	0.0426			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development	0.1113	Breast	0.0204
Gastrointestinal	0.0056	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0039	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0111
Hepatic	0.0000	Gastrointestinal	0.0244
Heart-blood vessels	0.0356	Hematopoietic	0.0000
Lung	0.0289	Skin-muscle	0.0065
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0062	Lung	0.0000
Placenta	0.1333	Nerves	0.0068
Prostate	0.0249	Prostate	0.0077
Sensory organs	0.0000	Sensory Organs	0.0125
		Uterus_n	

002221 00427960

## Electronic Northern for SEQ. ID NO.: 20

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0858	0.1048	0.8185	1.2217
Breast	0.1036	0.1729	0.5992	1.6690
Small intestine	0.1226	0.1158	1.0593	0.9441
Ovary	0.0958	0.1197	0.8009	1.2486
Endocrine tissue	0.0954	0.1128	0.8453	1.1830
Gastrointestinal	0.0900	0.1573	0.5725	1.7466
Brain	0.0658	0.0924	0.7120	1.4046
Hematopoietic	0.1109	0.0758	1.4645	0.6828
Skin	0.0918	0.0000	undef	0.0000
Hepatic	0.0333	0.0906	0.3676	2.7200
Heart	0.2120	0.0412	5.1398	0.1946
Testicles	0.0690	0.3625	0.1904	5.2509
Lung	0.0696	0.1186	0.5869	1.7040
Stomach-esophagus	0.0483	0.0460	1.0504	0.9520
Muscle-skeleton	0.0702	0.2820	0.2491	4.0145
Kidney	0.0652	0.1027	0.6344	1.5762
Pancreas	0.1140	0.1270	0.8974	1.1143
Penis	0.1018	0.0000	undef	0.0000
Prostate	0.1090	0.1277	0.8530	1.1723
Uterus-endometrium	0.1149	0.0000	undef	0.0000
Uterus-myometrium	0.0686	0.2106	0.3258	3.0692
Uterus-general	0.0458	0.1908	0.2402	4.1635
Breast hyperplasia	0.1279			
Prostate hyperplasia	0.1159			
Seminal vesicle	0.1157			
Sensory organs	0.1059			
White blood cells	0.0832			
Cervix	0.1278			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0136
Gastrointestinal	0.0557	Ovary_n	0.1595
Brain	0.2471	Ovary_t	0.0658
Hematopoietic	0.2199	Endocrine tissue	0.0000
Skin	0.1612	Fetal	0.0216
Hepatic	0.0000	Gastrointestinal	0.0732
Heart-blood vessels	0.1560	Hematopoietic	0.0057
Lung	0.2633	Skin-muscle	0.0259
Suprarenal gland	0.1012	Testicles	0.0000
Kidney	0.1014	Lung	0.1638
Placenta	0.1112	Nerves	0.0211
Prostate	0.0848	Prostate	0.0205
Sensory organs	0.3740	Sensory Organs	0.0000
	0.0126	Uterus_n	0.0333

09673400-122700

Electronic Northern for SEQ. ID NO.: 21

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0273	0.0102	2.6695	0.3746
Small intestine	0.0051	0.0019	2.7221	0.3674
Ovary	0.0276	0.0000	undef	0.0000
Endocrine tissue	0.0180	0.0000	undef	0.0000
Gastrointestinal	0.0136	0.0000	undef	0.0000
Brain	0.0134	0.0046	2.8992	0.3449
Hematopoietic	0.0015	0.0164	0.0900	11.1117
Skin	0.0053	0.0000	undef	0.0000
Hepatic	0.0147	0.0000	undef	0.0000
Heart	0.0048	0.0000	undef	0.0000
Testicles	0.0106	0.0412	0.2570	3.8912
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0052	0.0102	0.5080	1.9684
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0223	0.0060	3.7122	0.2694
Pancreas	0.0081	0.0000	undef	0.0000
Penis	0.0033	0.0276	0.1197	8.3571
Prostate	0.0030	0.0267	0.1123	8.9035
Uterus-endometrium	0.0022	0.0043	0.5118	1.9538
Uterus-myometrium	0.0135	0.0000	undef	0.0000
Uterus-general	0.0381	0.1019	0.3741	2.6732
Breast hyperplasia	0.0102	0.0000	undef	0.0000
Prostate hyperplasia	0.0032			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0130			
Cervix	0.0106			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0204
Gastrointestinal		Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0101
Hematopoietic	0.0111	Endocrine tissue	0.0490
Skin	0.0000	Fetal	0.0093
Hepatic	0.0157	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0057
Lung	0.0000	Skin-muscle	0.0421
Suprarenal gland	0.0107	Testicles	0.0154
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0010
Prostate	0.0247	Prostate	0.0274
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

004221 0042960

Electronic Northern for SEQ. ID NO.: 22

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder				
Breast	0.0000	0.0102	0.0000	undef
Small intestine	0.0064	0.0207	0.3093	3.2328
Ovary	0.0153	0.0662	0.2317	4.3157
Endocrine tissue	0.0180	0.0156	1.1513	0.8686
Gastrointestinal	0.0204	0.0351	0.5822	1.7176
Brain	0.0153	0.0231	0.6627	1.5090
Hematopoietic	0.0510	0.0257	1.9871	0.5032
Skin	0.0134	0.0000	undef	0.0000
Hepatic	0.0367	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0466	0.0000	undef	0.0000
Lung	0.0000	0.0117	0.0000	undef
Stomach-esophagus	0.0249	0.0348	0.7172	1.3943
Muscle-skeleton	0.0193	0.0077	2.5211	0.3967
Kidney	0.0377	0.0300	1.2564	0.7959
Pancreas	0.0244	0.0274	0.8922	1.1209
Penis	0.0083	0.0166	0.4986	2.0057
Prostate	0.0329	0.0267	1.2355	0.8094
Uterus-endometrium	0.0131	0.0149	0.8774	1.1397
Uterus-myometrium	0.0338	0.0000	undef	0.0000
Uterus-general	0.0000	0.0340	0.0000	undef
Breast hyperplasia	0.0153	0.0000	undef	0.0000
Prostate hyperplasia	0.0256			
Seminal vesicle	0.0238			
Sensory organs	0.0000			
White blood cells	0.0069			
Cervix	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0139	Ovary_n	0.3190
Brain	0.0194	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0039	Fetal	0.0373
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0114
Lung	0.0320	Skin-muscle	0.0680
Suprarenal gland	0.0434	Testicles	0.0231
Kidney	0.0000	Lung	0.0000
Placenta	0.0124	Nerves	0.0211
Prostate	0.0061	Prostate	0.0205
Sensory organs	0.0000	Sensory Organs	0.0077
	0.0251	Uterus_n	0.0458

002221.004E2960

Electronic Northern for SEQ. ID NO.: 23

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0741	0.0639	1.1593	0.8626
Breast	0.0691	0.0827	0.8352	1.1973
Small intestine	0.0245	0.0496	0.4943	2.0230
Ovary	0.0689	0.0494	1.3936	0.7176
Endocrine tissue	0.2487	0.5191	0.4791	2.0873
Gastrointestinal	0.0421	0.0879	0.4796	2.0852
Brain	0.1700	0.1037	1.6395	0.6099
Hematopoietic	0.0695	0.0758	0.9175	1.0899
Skin	0.0367	0.4237	0.0866	11.5419
Hepatic	0.0143	0.0388	0.3676	2.7200
Heart	0.0668	0.1375	0.4857	2.0588
Testicles	0.0460	0.0468	0.9839	1.0163
Lung	0.0592	0.0470	1.2590	0.7943
Stomach-esophagus	0.1160	0.0690	1.6807	0.5950
Muscle-skeleton	0.0754	0.0960	0.7853	1.2735
Kidney	0.0706	0.0479	1.4728	0.6790
Pancreas	0.0677	0.0552	1.2265	0.8153
Penis	0.0988	0.0267	3.7064	0.2698
Prostate	0.0697	0.0660	1.0566	0.9464
Uterus-endometrium	0.0608	0.0000	undef	0.0000
Uterus-myometrium	0.0152	0.0611	0.2494	4.0097
Uterus-general	0.1120	0.0000	undef	0.0000
Breast hyperplasia	0.0480	0.0565		
Prostate hyperplasia		0.0445		
Seminal vesicle		0.0823		
Sensory organs		0.0824		
White blood cells		0.0852		
Cervix				

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0544
Gastrointestinal	0.1113	Ovary_n	0.0000
Brain	0.0805	Ovary_t	0.0203
Hematopoietic	0.1376	Endocrine tissue	0.0245
Skin	0.1140	Fetal	0.0309
Hepatic	0.0000	Gastrointestinal	0.0610
Heart-blood vessels	0.0520	Hematopoietic	0.0000
Lung	0.0996	Skin-muscle	0.0356
Suprarenal gland	0.1951	Testicles	0.0077
Kidney	0.1268	Lung	0.0655
Placenta	0.1359	Nerves	0.0783
Prostate	0.1030	Prostate	0.0547
Sensory organs	0.0748	Sensory Organs	0.0000
	0.0879	Uterus_n	0.0083

002221" 004E/950



Electronic Northern for SEQ. ID NO.: 24

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0546	0.0332	1.6428	0.6087
Breast	0.0269	0.0320	0.8407	1.1896
Small intestine	0.0276	0.0000	undef	0.0000
Ovary	0.0479	0.0546	0.8771	1.1401
Endocrine tissue	0.0324	0.0176	1.8437	0.5424
Gastrointestinal	0.0211	0.0463	0.4556	2.1950
Brain	0.0229	0.0277	0.8266	1.2097
Hematopoietic	0.0348	0.0379	0.9175	1.0899
Skin	0.0194	0.0000	undef	0.0000
Hepatic	0.0190	0.0000	undef	0.0000
Heart	0.0477	0.0000	undef	0.0000
Testicles	0.0230	0.1169	0.1968	5.0816
Lung	0.0156	0.0307	0.5080	1.9684
Stomach-esophagus	0.0000	0.0460	0.0000	undef
Muscle-skeleton	0.0120	0.0480	0.2499	4.0023
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0182	0.0331	0.5484	1.8234
Penis	0.0180	0.0800	0.2246	4.4517
Prostate	0.0174	0.0170	1.0236	0.9769
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0229	0.0679	0.3367	2.9702
Uterus-general	0.0102	0.0000	undef	0.0000
Breast hyperplasia	0.0576			
Prostate hyperplasia	0.0208			
Seminal vesicle	0.0089			
Sensory organs	0.0118			
White blood cells	0.0277			
Cervix	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0278	Ovary_n	0.0000
Brain	0.0639	Ovary_t	0.0000
Hematopoietic	0.0438	Endocrine tissue	0.0000
Skin	0.0275	Fetal	0.0006
Hepatic	0.0000	Gastrointestinal	0.0122
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0925	Skin-muscle	0.0000
Suprarenal gland	0.0831	Testicles	0.0077
Kidney	0.0000	Lung	0.0000
Placenta	0.0803	Nerves	0.0040
Prostate	0.0667	Prostate	0.0000
Sensory organs	0.0249	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0000

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## Electronic Northern for SEQ. ID NO.: 25

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0429	0.0486	0.8832	1.1323
Breast	0.0435	0.0771	0.5643	1.7720
Small intestine	0.0307	0.0000	undef	0.0000
Ovary	0.0389	0.0833	0.4677	2.1381
Endocrine tissue	0.0460	0.0301	1.5283	0.6543
Gastrointestinal	0.0287	0.0971	0.2958	3.3803
Brain	0.0347	0.0534	0.6507	1.5367
Hematopoietic	0.0869	0.0000	undef	0.0000
Skin	0.0551	0.0847	0.6498	1.5389
Hepatic	0.0143	0.0194	0.7353	1.3600
Heart	0.0466	0.0137	3.3923	0.2948
Testicles	0.0173	0.0935	0.1845	5.4203
Lung	0.0457	0.0613	0.7451	1.3421
Stomach-esophagus	0.0290	0.0153	1.8908	0.5289
Muscle-skeleton	0.0223	0.1140	0.1954	5.1183
Kidney	0.0407	0.0137	2.9739	0.3363
Pancreas	0.0314	0.0442	0.7105	1.4075
Penis	0.0779	0.0533	1.4601	0.6849
Prostate	0.0458	0.0617	0.7412	1.3491
Uterus-endometrium	0.0473	0.0000	undef	0.0000
Uterus-myometrium	0.0305	0.1087	0.2806	3.5642
Uterus-general	0.0357	0.0954	0.3736	2.6765
Breast hyperplasia	0.0256			
Prostate hyperplasia	0.0803			
Seminal vesicle	0.0801			
Sensory organs	0.0118			
White blood cells	0.0494			
Cervix	0.0426			

002221-004E2950

	FETUS % frequency	STANDARDIZED/SUBTRACTED LIBRARIES % frequency	
Development		Breast	0.0204
Gastrointestinal	0.0417	Ovary_n	0.1595
Brain	0.0611	Ovary_t	0.0101
Hematopoietic	0.0626	Endocrine tissue	0.0000
Skin	0.0708	Fetal	0.0332
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0260	Hematopoietic	0.0000
Lung	0.0534	Skin-muscle	0.0194
Suprarenal gland	0.0542	Testicles	0.0077
Kidney	0.0761	Lung	0.0328
Placenta	0.0988	Nerves	0.0161
Prostate	0.0303	Prostate	0.0068
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0251	Uterus_n	0.0291

## Electronic Northern for SEQ. ID NO.: 26

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	3.0675	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0015	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0000	0.0000	undef	undef
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0000			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

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FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development		Breast	0.0000
Gastrointestinal		Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0028	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0070
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0000
Prostate	0.0061	Prostate	0.0155
Sensory organs	0.0000	Sensory Organs	0.0250
	0.0000	Uterus_n	

Electronic Northern for SEQ. ID NO.: 27

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0039	0.0230	0.1695	5.8999
Breast	0.0179	0.0395	0.4537	2.2042
Small intestine	0.0061	0.0000	undef	0.0000
Ovary	0.0300	0.0130	2.3025	0.4343
Endocrine tissue	0.0068	0.0251	0.2717	3.6805
Gastrointestinal	0.0077	0.0093	0.8283	1.2072
Brain	0.0015	0.0092	0.1600	6.2504
Hematopoietic	0.0053	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0194	0.0000	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0083	0.0368	0.2258	4.4288
Stomach-esophagus	0.0290	0.0230	1.2605	0.7933
Muscle-skeleton	0.0000	0.0060	0.0000	undef
Kidney	0.0136	0.0068	1.9826	0.5044
Pancreas	0.0000	0.0276	0.0000	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0065	0.0128	0.5118	1.9538
Uterus-endometrium	0.0473	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0051	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix	0.0213			

FETUS  
% frequency

STANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0139	Ovary_n	0.0000
Brain	0.0278	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0304
Skin	0.0079	Fetal	0.0245
Hepatic	0.0000	Gastrointestinal	0.0029
Heart-blood vessels	0.0000	Hematopoietic	0.0122
Lung	0.0320	Skin-muscle	0.0114
Suprarenal gland	0.0289	Testicles	0.0097
Kidney	0.0000	Lung	0.0000
Placenta	0.0185	Nerves	0.0164
Prostate	0.0000	Prostate	0.0020
Sensory organs	0.0997	Sensory Organs	0.0068
	0.0000	Uterus_n	0.0000

00673400 122700

Electronic Northern for SEQ. ID NO.: 28

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0195	0.0383	0.5085	1.9666
Breast	0.0256	0.0714	0.3582	2.7919
Small intestine	0.0552	0.0331	1.6683	0.5994
Ovary	0.0270	0.0468	0.5756	1.7372
Endocrine tissue	0.0477	0.0451	1.0566	0.9464
Gastrointestinal	0.0326	0.0324	1.0058	0.9942
Brain	0.0503	0.0277	1.8132	0.5515
Hematopoietic	0.0201	0.1894	0.1059	9.4460
Skin	0.0367	0.2542	0.1444	6.9252
Hepatic	0.0476	0.0388	1.2255	0.8160
Heart	0.0699	0.0550	1.2721	0.7861
Testicles	0.0173	0.1403	0.1230	8.1305
Lung	0.0395	0.0818	0.4826	2.0720
Stomach-esophagus	0.0676	0.0613	1.1030	0.9066
Muscle-skeleton	0.0394	0.0300	1.3135	0.7613
Kidney	0.0462	0.0616	0.7490	1.3351
Pancreas	0.0347	0.0607	0.5711	1.7510
Penis	0.0509	0.1600	0.3182	3.1424
Prostate	0.0327	0.0149	2.1935	0.4559
Uterus-endometrium	0.0000	0.0000	undef	undef
Uterus-myometrium	0.0076	0.0543	0.1403	7.1284
Uterus-general	0.0357	0.0000	undef	0.0000
Breast hyperplasia	0.0192			
Prostate hyperplasia	0.0565			
Seminal vesicle	0.0445			
Sensory organs	0.0941			
White blood cells	0.0390			
Cervix	0.0319			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	
Gastrointestinal	0.0557	Ovary_n	0.0340
Brain	0.0194	Ovary_t	0.0000
Hematopoietic	0.0188	Endocrine tissue	0.0101
Skin	0.0197	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0396
Heart-blood vessels	0.0000	Hematopoietic	0.0244
Lung	0.0320	Skin-muscle	0.0000
Suprarenal gland	0.0325	Testicles	0.0778
Kidney	0.0000	Lung	0.0000
Placenta	0.0371	Nerves	0.0231
Prostate	0.0242	Prostate	0.0479
Sensory organs	0.0997	Sensory Organs	0.0697
	0.0000	Uterus_n	0.0291

002227 00437600

## Electronic Northern for SEQ. ID NO.: 29

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0663	0.0358	1.8523	0.5399
Breast	0.0512	0.0489	1.0470	0.9551
Small intestine	0.0368	0.0496	0.7415	1.3487
Ovary	0.0779	0.0728	1.0690	0.9354
Endocrine tissue	0.0562	0.0326	1.7242	0.5800
Gastrointestinal	0.0345	0.0370	0.9319	1.0731
Brain	0.0392	0.0524	0.7482	1.3366
Hematopoietic	0.0602	0.0379	1.5880	0.6297
Skin	0.0587	0.0000	undef	0.0000
Hepatic	0.0095	0.0647	0.1471	6.7999
Heart	0.0583	0.0550	1.0601	0.9433
Testicles	0.0173	0.1520	0.1135	8.8080
Lung	0.0208	0.0491	0.4234	2.3620
Stomach-esophagus	0.0387	0.0460	0.8404	1.1900
Muscle-skeleton	0.0360	0.0420	0.8567	1.1673
Kidney	0.0380	0.0616	0.6168	1.6213
Pancreas	0.0314	0.0884	0.3552	2.8150
Penis	0.0689	0.0267	2.5833	0.3871
Prostate	0.0436	0.0490	0.8901	1.1235
Uterus-endometrium	0.0541	0.0000	undef	0.0000
Uterus-myometrium	0.0381	0.1155	0.3301	3.0296
Uterus-general	0.0815	0.0000	undef	0.0000
Breast hyperplasia	0.0831			
Prostate hyperplasia	0.0446			
Seminal vesicle	0.0801			
Sensory organs	0.0353			
White blood cells	0.0520			
Cervix	0.0532			

FETUS  
% frequencySTANDARDIZED/SUBTRACTED  
LIBRARIES  
% frequency

Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.1595
Brain	0.0389	Ovary_t	0.0203
Hematopoietic	0.0188	Endocrine tissue	0.0000
Skin	0.0472	Fetal	0.0093
Hepatic	0.0000	Gastrointestinal	0.0366
Heart-blood vessels	0.0260	Hematopoietic	0.0000
Lung	0.0498	Skin-muscle	0.0130
Suprarenal gland	0.0614	Testicles	0.0000
Kidney	0.0254	Lung	0.0164
Placenta	0.0741	Nerves	0.0120
Prostate	0.0364	Prostate	0.0205
Sensory organs	0.0499	Sensory Organs	0.0000
	0.0000	Uterus_n	0.0208

002221" 004E 2966

Electronic Northern for SEQ. ID NO.: 30

	NORMAL	TUMOR	Ratios	
	% frequency	% frequency	N/T	T/N
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0013	0.0000	undef	0.0000
Small intestine	0.0092	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0034	0.0000	undef	0.0000
Gastrointestinal	0.0019	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0010	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidney	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0109	0.0021	5.1181	0.1954
Prostate	0.0000	0.0000	undef	undef
Uterus-endometrium	0.0000	0.0340	0.0000	undef
Uterus-myometrium	0.0102	0.0000	undef	0.0000
Uterus-general	0.0000			
Breast hyperplasia	0.0000			
Prostate hyperplasia	0.0089			
Seminal vesicle	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			
Cervix				

002221" 00452950

FETUS		STANDARDIZED/SUBTRACTED LIBRARIES	
	% frequency		% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0000	Ovary_t	0.0000
Hematopoietic	0.0000	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0000	Skin-muscle	0.0000
Suprarenal gland	0.0000	Testicles	0.0000
Kidney	0.0000	Lung	0.0000
Placenta	0.0000	Nerves	0.0068
Prostate	0.0000	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
		Uterus_n	

Electronic Northern for SEQ. ID NO.: 31

	NORMAL % frequency	TUMOR % frequency	Ratios N/T	T/N
Bladder	0.0000	0.0051	0.0000	undef
Breast	0.0038	0.0019	2.0416	0.4898
Small intestine	0.0031	0.0000	undef	0.0000
Ovary	0.0030	0.0104	0.2878	3.4745
Endocrine tissue	0.0034	0.0100	0.3396	2.9444
Gastrointestinal	0.0057	0.0046	1.2425	0.8048
Brain	0.0111	0.0051	2.1599	0.4630
Hematopoietic	0.0040	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0048	0.0000	undef	0.0000
Heart	0.0095	0.0000	undef	0.0000
Testicles	0.0058	0.0000	undef	0.0000
Lung	0.0042	0.0102	0.4064	2.4605
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5711	1.7510
Kidney	0.0163	0.0068	2.3791	0.4203
Pancreas	0.0017	0.0000	undef	0.0000
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0022	0.0021	1.0236	0.9769
Uterus-endometrium	0.0135	0.0000	undef	0.0000
Uterus-myometrium	0.0000	0.0340	0.0000	undef
Uterus-general	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0224			
Prostate hyperplasia	0.0030			
Seminal vesicle	0.0089			
Sensory organs	0.0000			
White blood cells	0.0061			
Cervix	0.0213			

STANDARDIZED/SUBTRACTED  
LIBRARIES

	FETUS % frequency		% frequency
Development		Breast	0.0000
Gastrointestinal	0.0000	Ovary_n	0.0000
Brain	0.0028	Ovary_t	0.0000
Hematopoietic	0.0125	Endocrine tissue	0.0000
Skin	0.0000	Fetal	0.0000
Hepatic	0.0000	Gastrointestinal	0.0000
Heart-blood vessels	0.0000	Hematopoietic	0.0000
Lung	0.0036	Skin-muscle	0.0000
Suprarenal gland	0.0036	Testicles	0.0000
Kidney	0.0254	Lung	0.0082
Placenta	0.0062	Nerves	0.0000
Prostate	0.0303	Prostate	0.0000
Sensory organs	0.0000	Sensory Organs	0.0000
	0.0126	Uterus_n	0.0000

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Electronic Northern for Seq. ID: 52

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma			
Bladder	0.0599	0.0543	1.1037 0.9060
Breast	0.0507	0.0282	1.7979 0.5562
Large intestine	0.0326	0.0450	0.7240 1.3811
Small intestine	0.0268	0.0313	0.8563 1.1679
Ovary	0.0439	0.0426	1.0306 0.9703
Endocrine tissue	0.0564	0.0453	1.2443 0.8037
Brain	0.0642	0.0530	1.2113 0.8255
Skin	0.0380	0.0379	1.0022 0.9978
Hepatic	0.0330	0.0789	0.4190 2.3868
Heart	0.0093	0.0508	0.1831 5.4614
Testicles	0.0589	0.0000	undef 0.0000
Lung	0.0482	0.0533	0.9047 1.1054
Stomach-esophagus	0.0389	0.0499	0.7796 1.2828
Muscle-skeleton	0.0072	0.0256	0.2833 3.5296
Kidney	0.0240	0.0702	0.3418 2.9256
Pancreas	0.0694	0.0289	2.3984 0.4169
Prostate	0.0297	0.0331	0.8974 1.1143
T lymphoma	0.0443	0.0287	1.5457 0.6470
Uterus	0.0505	0.1643	0.3074 3.2533
White blood cells	0.0325	0.0690	0.4715 2.1210
Hematopoietic	0.0363	0.0304	1.1948 0.8370
Penis	0.0495		
Seminal vesicle	0.0322		
Sensory organs	0.0493		
	0.0470		

FETUS  
% freq.

Development	0.0696
Gastrointestinal	0.0750
Brain	0.0876
Hematopoietic	0.0904
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0854
Lung	0.0867
Adrenal gland	0.0761
Kidney	0.0556
Placenta	0.0606
Prostate	0.0499
Sensory organs	0.0628

STANDARDIZED/SUBTRACTED LIBRARIES  
% frequency

Breast	
Breast t	0.0068
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.1595
Endocrine tissue	0.0101
Fetal	0.0245
Gastrointestinal	0.0284
Hematopoietic	0.0732
Skin-muscle	0.0000
Testicles_n	0.0616
Testicles_t	0.0293
Lungs_n	0.0000
Lungs_t	0.0195
Nerves	0.0000
Kidney t	0.0261
Ovary uterus	0.0000
Prostate_n	0.0293
Sensory organs	0.0121
White blood cells	0.0310
	0.0000

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## 2.2. Fisher Test

In order to decide whether a partial sequence  $S$  of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to  $S$ . If the null hypothesis can be rejected with high enough certainty, the gene belonging to  $S$  is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

### Example 3

#### Automatic Lengthening of the Partial Sequence

Automatic lengthening of partial sequence  $S$  is completed in three steps:

1. Determination of all sequences homologous to  $S$  from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program  
GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence  $C$  from the assembled sequences.

Consensus sequence  $C$  will generally be longer than initial sequence  $S$ . Its electronic Northern Blot will accordingly

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deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences  $C_i$  (i: iteration index) obtained in each case until the alternative hypothesis is rejected (if  $H_0$  Exit; truncation criterion I) or until automatic lengthening is no longer possible (while  $C_i > C_{i-1}$ ; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from hysteryomic tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORF's) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

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**Example 4****Mapping of Nucleic Acid Sequences on the Human Genom**

Sub B1
 Human genes were mapped using the Stanford G3 Hybrid Panel (Stewart et al., 1997), which is marketed by Research Genetics, Huntsville, Alabama. This panel consists of 83 different genomic DNAs of human-hamster hybrid cell lines and allows resolution of 500 kilobases. The hybrid cell lines were obtained by fusion of irradiated diploid human cells with cells of the Chinese hamster. The retention pattern of the human chromosome fragments is determined by means of gene-specific primers in a polymerase chain reaction and is analyzed using software available from the Stanford RH server ([http://www.stanford.edu/RH/rhserver\\_form2.html](http://www.stanford.edu/RH/rhserver_form2.html)). This program determines the STS marker that is nearest to the desired gene. The corresponding cytogenetic band was determined using the "Mapview" program of the Genome Database (GDB), (<http://gdbwww.dkfz-heidelberg.de>).

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the Gap between Genome Mapping and Genome

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Sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence Mapping by Electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

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the results were evaluated with the above-mentioned software and  
the software of the Whitehead Institute  
(<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

B  
cont.

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TABLE I

Col. 1 - Sequence ID No.:

Col. 2 - Expression in hysteromyomic tissue:

Col. 3 - Function

Col. 4 - Modules

Col. 5 - Length of the applied sequence in bases

Col. 6 - Cytogenetic localization

Col. 7 - Next marker

[Key to Table I:]

[Col. 2:] erhöht = elevated

[Col. 3:]

[Seq. ID No.: 14, 15, 17, 30, 31] unbekannt = unknown

[Seq. ID No.: 16] Homolog zu Homo sapiens... = homologous  
to homo sapiens...

[Seq. ID No.: 18] Humanes Homolog zu ... = human homolog to

[Seq. ID No.: 52] Verlängerung von Seq. ID. 14 =  
Lengthening of Seq. ID. 14B' cont.  
00/222T" 004E2960

TABLE I

Sequenz ID No.	Expression im Uterus-Myomgewebe:	Funktion	Module	Länge der angemeldeten Sequenz in Basen	Cygenetische Lokalisation	nächster Marker
1	erhöht	Human mRNA for ornithine decarboxylase antizyme	"abhydro-lase"	779		
2	erhöht	Human MEST mRNA		2310		
3	erhöht	Human cocaine and amphetamine regulated transcript CART (hCART)		854	5q11.2-q13.1	D5S1730
4	erhöht	Human microfibril-associated glycoprotein (MFAP2)		1112	1p36.11-p36.13	
5	erhöht	Human mRNA for KIAA0108 gene		1051	2p23.3	D2S387
6	erhöht	Human SPARC/osteonectin	"kazal"	1516	5q32-q33.1	
7	erhöht	Human sapiens splicing factor, arginine/serine-rich 7 (SFRS7)	"rrm"	2367	2p22.3-p22.1	WI-9798
8	erhöht	Human triosephosphate isomerase	3x "TIM"	568		
9	erhöht	Human nuclear ribonucleoprotein particle (hnRNP) C	"Thymosin"	1775		
10	erhöht	Human thymosin beta-4	"IGFBP"	509		
11	erhöht	Human growth hormone-dependent insulin-like growth factor-binding protein mRNA	"Ihro-globulin_1"	2191	7p12.2-p13	
12	erhöht	Human H19		1769		
13	erhöht	Human cellular retinoic acid-binding protein II (CRABP)	"lipocalin"	1026		
14	erhöht	unbekannt	"rrm"	676	14p11.2-14p11.1	WI-4204
15	erhöht	unbekannt		1254		
16	erhöht	Homolog zu Homo sapiens mRNA for putatively prenylated protein		537		
17	erhöht	unbekannt		823		
18	erhöht	Humanes Homolog zu P. vivax pva1 gene		1082		
19	erhöht	Human lumican mRNA	5x "LRR"	1548	12q21.31-12q21.33	D12S351
20	erhöht	Human 37 kD laminin receptor precursor/p40 ribosome associated protein	"S2"	844		
21	erhöht	Human YMP	"PMP22"	862		
22	erhöht	Human NADH:ubiquinone oxidoreductase MLRQ subunit		546		
23	erhöht	Human mRNA for coupling protein G(s) alpha-subunit	"G-alpha", "arf"	1591	20q13.32-q13.33	
24	erhöht	Human hnRNP core protein A1	"rrm"	441		
25	erhöht	Human HMG-17 gene for non-histone chromosomal protein	"HMG14_17"	1131		
26	erhöht	H sapiens mRNA for prolactin (clone PRL205)	"hormone"	1071		
27	erhöht	Human mRNA for neurite outgrowth-promoting protein.	3x "PTN MK"	896		
28	erhöht	H sapiens mRNA for proliferation-associated gene (pag)	"AhpC-TSA"	1050	1p32.3-p34.3	
29	erhöht	H sapiens alpha NAC		581		
30	erhöht	unbekannt		264		
31	erhöht	unbekannt		111		
52	erhöht	Verlängerung von Seq. ID. 14	"rrm"	3665	14p11.2-14p11.1	WI-4204

## References to the modules:

Pfam: Protein families database of alignments and HMMs  
(pfam@sanger.ac.uk)

PROSITE: The PROSITE database, its status in 1999. Nucleic  
Acids Res. 27: 215-219 (<http://www.expasy.ch/sprot/prosite.html>)

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TABLE II

## DNA Sequences

## Peptide Sequences (ORF's)

Seq. ID. No.

Seq. ID. No.

14

32

33

34

15

35

36

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16

38

39

17

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41

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The inventive nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 31 of the determined candidate genes and the determined amino acid sequences Seq. ID No. 32 to Seq. ID No. 51 are described in the following sequence protocol.

### Sequence Protocol

#### (1) GENERAL INFORMATION:

##### (i) APPLICANT:

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1673
- (H) FAX: (030)-8413 1674

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Hysteromyomic Tissue

(iii) Number of sequences: 55

##### (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

002227 004E2960

## (2) INFORMATION ON SEQ ID NO. 1:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 779 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```

agcgagcagc ggcggcggcg cggagagacg cagcggaggt ttctctgggt tcggacccca 60
gcggccggat ggtgaaatcc tccctgcagc ggatcctcaa tagccactgc ttcgccagag120
agaaggaagg ggataaacc agcgccacca tccacgccag ccgcaccatg ccgtccta180
gcctgcacag ccgcggcggc agcagcagtg agagtccag ggtctccctc cactgctgta240
gtaacccggg tccggggcct cggtggtgct cctgatgcc ctcacccacc cctgaagatc300
ccagggtggg gaggggaatag tcaaagggac cacaatcttc cagctaactt attctactcc360
gatgatcggc tgaatgtaac agaggaacta acgtccaacg acaagacgag gattctcaac420
gtccagtcca ggctcacaga cgccaaacgc attactggc gaacagtgct gagtggcggc480
actgctctac atcgagatcc cgggcggcg cgtgcccgag gggagcaagg acagctttgc540
agttctcctg ggagttcgct gaggagcagc tgcgaggccg accatgtctt aatttgcttc600
cacaagaacc ccgaggacag agccgccttg ctccgaacct tcagcttttt cgggcttgag660
atcttgagac cggggcatcc cctttgttcc ccaagagacc cgacgcttgc ttcattgggc720
tacaagtctc gagagagagt ctttggggag aggaagaagg attaggggcc gcgtcgggt 779

```

## (2) INFORMATION ON SEQ ID NO. 2:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2310 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

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(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

gtttctccgaa acatggagtc ctgtaggcaa ggtctttacct gaatcaggat gagggagtg 60
tgggtccagg tggggctgct ggccgtgccc ctgcttgctg cgtacctgca catcccaccc 120
cctcagcgct cccctgcccc tcaactcatgg aagtcttcag gcaagttttt cacttacaag 180
ggactgcgta tcttctacca agactctgtg ggtgtggttg gaagtccaga gatagtgtg 240
cttttacacg gttttccaac atccagctac gactggtaca agatttgga aggtctgacc 300
ttgaggtttc atcgggtgat tggccttgat ttcttaggct ttggcttcag tgacaaaccg 360
agaccacatc actattccat atttgagcag gccagcatcg tggaaagcgt ttgcgggcat 420
ctggggctcc agaaccgcag gatcaacctt ctttctcatg actatggaga tattgttgct 480
caggagcttc tctacaggta caagcagaat cgatctggtc ggcttaccat aaagagtctc 540
tgtctgtcaa atggaggtat ctttctctgag actcacgcgc cactccttct ccaaaagcta 600
ctcaaagatg gaggtgtgct gtcacccatc ctcacacgac tgatgaactt ctttgtattc 660
tctcgaggtc tcaccccagt ctttggggccg tatactcggc cctctgagag tgagctgtgg 720
gacatgtggg cagggatccg caacaatgac gggaaacttag tcattgacag tctcttacag 780

tacatcaatc agaggaagaa gttcagaagg cgctgggttg gagctcttgc ctctgtaact 840
atccccattc attttatcta tgggccattg gatccttcaa atccctatcc agagtttttg 900
gagctgtaca ggaaaacgct gccgcgggtcc acagtgtgga ttctggatga ccacattagc 960
cactatccac agctagagga tcccatgggc ttcttgaatg catatatggg cttcatcaac 1020
tccttctgag ctggaaagag tagcttccct gtattacctc cctactccc ttatgtgttg 1080
tgtattccac ttaggaagaa atgccccaaa gaggtcctgg ccatcaaaca taattctctc 1140
acaaagtcca ctttactcaa attggtgaac agtgtatagg aagaagccag caggagctct 1200
gactaagggt gacataatag tccacctccc attactttga tatctgatca aatgtataga 1260
cttggctttg tttttgtgc tattaggaaa ttctgatgag cattactatt cactgatgca 1320
gaaagacgtt cttttgcata aaagactttt tttaacactt tggacttctc tgaaatattt 1380
agaagtgtca atttctggcc ccccccaac aggaattcta tagtaagggg gaggagaagg 1440
ggggctcctt cctctcctc gaatgacgtt atgggcacat gcctttttaa agttctttta 1500
gcaacacaga gctgagtcct ctttgtcata cttttggatt tagtgtttca tcagctgttt 1560
ttagttataa acattttgtt aaaatagata ttggtttaaa tgatacagta ttttaggtat 1620
gatttaagac tatgatttac ctatacatTA tatatatTT ataaagatac taaaccagca 1680
taccttact ctgccagagt agtgaagcta attaaacacg tttggtttct gaataaattg 1740
aactaaatcc aaactatttc ctaaaatcac aggacattaa ggaccaatag catctgtgcc 1800
agagatgtac tgttatttagc tgggaagacc aattctaaca gcaaataaca gtctgagact 1860
cctcatacct cagtggttag aagcatgtct ctcttgagct acagttagag ggaagggatt 1920
gtrgtgtagt caagtcacca tgctgaatgt acactgattc ctttatgatg actgcttaac 1980
tccccactgc ctgtcccaga gaggttttcc aatgtagctc agtaattcct gttactttac 2040
agacaggaaa gttccagaaa ctttaagaac aaactctgaa agacctatga gcaaattgg 2100
ctgaataact tttttttaaa gccacatttc attgtcttag tcaaagcagg attattaaq 2160
gattatttaa aattcgtttt tttaaattag caacttcaag tataacaact ttgaaactgg 2220
aataagtgtt tattttctat taataaaaaat gaattgtgac aaaaaaaaaa aaaggcttcg 2280
gcttttgaag tctatgtgtg gggggggggg
2310

```

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## (2) INFORMATION ON SEQ ID NO. 3:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 854 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

ctgcacgggg gctcggggctc actataaaaag gtgggagcgc gtggtgcccc agcaacgacg 60
agtttcagaa cgatggagag ctcccgcgtg aggcctgctgc ccttcctggg cgccgccctg120
ctgctgatgc tacctctgtt gggtagccgt gccaggagg acgccgagct ccagccccga180
gccctggaca tctactctgc cgtggatgat gcctcccacg agaaggagct gatcgaagcg240
ctgcaagaag tcttgaagaa gctcaagagt aaacgtgttc ccatctatga gaagaagtat300

ggccaagtcc ccatgtgtga cgccggtgag cagtgtgcag tgaggaaaagg ggcaaggatc360
gggaagctgt gtgactgtcc ccgaggaacc tcttgcaatt ccttcctcct gaagtgtta420
tgaagggggc gccattctcc tccatacatc cccatccctc tactttcccc agaggaccac480
accttcctcc ctggagtttg gcttaagcaa cagataaagt ttttattttc ctctgaagg540
aaagggctct tttcctgctg tttcaaaaat aaaagaacac attagatgtt actgtgtgaa600
gaataatgcc ctgtatgggt ttgatacgtg tgtgaagtat tcttatttta tttgtctgac660
aaactcttgt gtacctttgt gtaaagaagg gaagctttgt ttgaaaattg tatttttgt720
tgtggcatgg cagaatgaaa attagatcta gctaattctg gtagatgtca ttacaacctg780
gaaaataaat caccctaagt gacacaaatt gaagcatgta caaattatac ataataaagt840
gtttttaata attg

```

## (2) INFORMATION ON SEQ ID NO. 4:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1112 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

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(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

cgccagcccc gtcggggggcc cggagggggac tcggagcggg ccaagggggcg gctccggcgg 60  
gcggactcgg agcggggcggc ggagtgaccc ggacagctgt cctctctgac accaccccgg 120  
cctgcctctt tgttgccatg agagctgcct acctcttctt gctattcctg cctgcaggct 180  
tgctggctca gggccagtat gacctggacc cgctgccgcc gttccctgac cacgtccagt 240  
acacccacta tagcgaccag atcgacaacc cagactacta tgattatcaa gaggtgactc 300  
ctcggccctc cgaggaacag ttccagttcc agtcccagca gcaagtccaa caggaagtca 360  
tcccagcccc aaccccagaa ccaggaaatg cagagctgga gcccacagag cctgggcctc 420  
ttgactgccg tgaggaacag taccctgtgca cccgcctcta ctccatacac aggccttgca 480  
aacagtgtct caacgagggtc tgcttctaca gcctccgccg tgtgtacgtc attaacaagg 540  
agatctgtgt tcgtacagtg tgtgcccatt aggagctcct ccgagctgac ctctgtcggg 600  
acaagtcttc caaatgtggc gtgatggcca gcagcggcct gtgccaatcc gtggcggcct 660  
cctgtgccag gagctgtggg agctgctagg gtggtgctgg catcctgagt cctggccctc 720  
ctgggatctg gggccctcgg gccctgcctg acctggtgt tttttcccca tccccatgtt 780  
cctttttattc tgtaaaaagt tagtggaactg cagccctggg gggtgcaggc tgcggtgcct 840  
caggcccttc cttcagcctg tggccacctc tggggcacga tgggggctcc ccactgcca 900  
gtctgcccct cgggttgggg gagtatccca ggcctctctg tgggacctg ggccctgacg 960  
ggccttctca gcccgttttg aggacagaca gtcccccgag gtaggctaca tccccccacc 1020  
ccagctggtc tgcttgatt tcctacagcc cccgtgggca tggaccacct ttattttatal 1080  
caaaattaaa aacaagtttt tacaaaaaaa aa 1112

(2) INFORMATION ON SEQ ID NO. 5:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1051 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

09673400-122700

## (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

gcgcaggcgc gaagaagctg gcagggggcac gagccggggg cggggttgaa gacgcgtcgt 60
tgggttttgg aggccgtgaa acagccgttt gagtttggct gcgggtggag aacgtttgtc 120
agggggcccg ccaagaagga ggccgcctg ttacgatggt gtccatgagt ttcaagcgga 180
accgcagtga ccggttctac agcaccgggt gctgcggctg ttgccatgtc cgcaccggga 240
cgatcatcct ggggacctgg tacatggtag taaacctatt gatggcaatt ttgctgactg 300
tggaagtgac tcatccaaac tccatgccag ctgtcaacat tcagtatgaa gtcacggta 360
attactattc gtctgagaga atggctgata atgcctgtgt tctttttgcc gtctctgttc 420
ttatgtttat aatcagttca atgctggttt atggagcaat ttcttatcaa gtgggttggc 480
tgattccatt cttctgttac cgactttttg acttcgtcct cagttgcctg gttgctatta 540
gttctctcac ctatttgcca agaatcaaag aatatctgga tcaactacct gattttccct 600
acaaagatga cctcctggcc ttggactcca gctgcctcct gttcattgtt cttgtgttct 660
ttgccttatt catcattttt aaggcttatt taattaactg tgtttggaac tgctataaat 720
acatcaacaa ccgaaacgtg ccggagattg ctgtgtaccc tgcttttgaa gcacctctc 780
agtacgtttt gccaacctat gaaatggccg tgaaaatgcc tgaaaaagaa ccaccacctc 840
cttacttacc tgcctgaaga aattctgcct ttgacaataa atcctatacc agctttttgt 900
ttgtttatgt tacagaatgc tgcaattcag ggctcttcaa acttgtttag atataaaata 960
tggtggccct ttggttttaa agcaatttat ttccaaaac actaaggag ccttttttga 1020
catctgggta aacggccttt ttgggttttt t

```

1051

## (2) INFORMATION ON SEQ ID NO. 6:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1516 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

gttgctcctca tccctctcat acaggggtgac caggacgttc ttgagccagt cccgcatgcg 60
caggggggaag aagatccatg agaaggagaa gcgcctggag gcaggagacc accccgtgga 120
gctgctggcc cgggacttcg agaagaacta taacatgtac atcttccctg tacactggca 180
gttcggccag ctggaccagc accccattga cgggtacctc tcccacaccg agctggctcc 240
actgctgct cccctcatcc ccatggagca ttgaccacc cgcttttttcg agacctgtga 300
cctggacaat gacaagtaca tcgccctgga tgagtgggcc ggctgcttcg gcatcaagca 360
gaaggataatc gacaaggatc ttgtgatcta aatccactcc ttcacacagta ccggattctc 420
tctttaaccc tcccttctgt gtttccccc atgtttaaaa tgtttggatg gtttgttgtt 480
ctgcctggag acaagggtgct aacatagatt taagtgaata cattaacggg gctaaaaatg 540
aaaattctaa cccaagaaca tgacattctt agctgtaact taactattaa ggctttttcc 600
acacgcatta atagtcccat ttttctcttg ccatttgtag ctttgcccat tgtcttattg 660
ggcacatggg gtggacacgg atctgctggg ctctgcctta aacacacatt gcagcttcaa 720
cttttctctt tagtgttctg tttgaaacta atacttaccg agtcagactt tgtgttcatt 780
tcatttcagg gtcttggctg cctgtgggct tcccaggtg gcctggaggt gggcaaaggg 840
aagtaacaga cacacgatgt tgtcaaggat ggttttggga ctagaggctc agtggtgga 900
gagatccctg cagaacccac caaccagaac gtggtttgct tgaggctgta actgagagaa 960
agattctggg gctgtgttat gaaaatatag acattctcac ataagcccag ttcacaccal1020
tttctctctt tacctttcag tgcagtttct tttcacatta ggctgttggg tcaaaccttt1080
gggagcacgg actgtcagtt ctctgggaag tggtcagcgc atcctgcagg gcttctctcl1140
ctctgtcttt tggagaacca gggctcttct caggggctct agggactgcc aggctgtttcl1200
agccaggaag gccaaaatca agagtgaat gttagaaagt gtaaaaataga aaaagtggag1260
ttggtgaatc ggttgttctt tcttcacatt tggatgattg tcataagggt tttagcatgt1320
tctctctttt ctccaccctc cccttttttc cccaagaat acagagaaaa ctcaaagtta1380
atggggaggg tcggatccta caggcctgag aatcggtcaa ctccaagcat ttcattgaaa1440
agggcgcttc ctaattaatc ctacaaaccc ccaccagga tggtgagggg tttcaccaat1500
tcttccaaaa ataaaa

```

1516

## (2) INFORMATION ON SEQ ID NO. 7:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2367 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

cgccgggact cttggcgggt gaaggtgtgt gtcagctttt gcgtcactcg agccctgggc 60  
gctgcttgct aaagagccga gcacgcgggt ctgtcatcat gtcgcgttac gggcgggtacg 120  
gaggagaaac caaggtgtat gttggttaacc tgggaactgg cgctggcaaa ggagagttag 180  
aaagggtttt cagttattat ggtcctttta gaactgtatg gattgcgaga aatcctccag 240  
gatttgcttt tgtggaattc gaagatccta gagatgcaga agatgcagta cgaggactgg 300  
atggaaaggt gatttgtggc tcccagagtga gggttgaact atcgacaggc atgcctcgga 360  
gatcacgttt tgatagacca cctgcccgcac gtccctttga tccaaatgat agatgctatg 420  
agtgtggcga aaaggacat tatgcttatg attgtcatcg ttacagccgg cgaagaagaa 480  
gcaggtcacg gtctagatca cattctcgat ccagagggaag gcgatactct cgctcacgca 540  
gcaggagcag gggacgaagg tcaaggtcag catctcctcg acgatcaaga tctatctctc 600  
ttcgragatc aagatcagct tcaactcagaa gatctaggtc tggttctata aaaggatcga 660  
ggtattttcca atccccgtcg aggtcaagat caagatccag gtctatttca cgaccaagaa 720  
gcagccgatac aaagtcacga tctccatctc caaaaagaag tcgttcccca tcagggaagtc 780  
ctcgcaagaag tgcaagtcct gaaagaatgg actgaagctc tcaagttcac cctttaggga 840  
aaagttattt tgtttacatt attataaggg atttgtgatg tctgtaaaagt gtaacctagg 900  
aaagataatt caaccatcta atcaaaatgg atctggatta ctatgtaaat tcacagcagt 960  
aagataatat aaattttgtt gaatgtatta acatcatatg gtctgaaaat gtgggttttt1020  
atlttggcaca tttaaataaa atgtttctaa ctagattttt gatttgtgtt caatattaac1080  
acttcttaat ttgaratatt tgagagtcag acattataat tgtaaacctt attcatacat1140  
acctatgaa agaatgaaa ggtgttgggt aagtcctgaa catcactatt ctatgcataa1200  
aacttggcca ggatcttaag ggactttgaa aattccatct tacccttgta gctctgggta1260  
agatgacctg agtcccttat gatacagcct gaatgcacat tgacagatcc ttaagttagc1320  
taatccgttt gaagttgggt ttagtaggta ttgtatgatc agtgggtgaag caagtaggac1380  
cactgatgtg tctaaatgag catgacagga actaaacgaa actgattaaa tgtatgagaa1440  
atagaaactg atttctggat gatctttata ctaattgcag ctttcaggct actaggtggc1500  
atagtgttaa ttaggactcc ccaagatatg gggagttcta ctctcaatgg tcttgtttct1560  
ttgctttcta cattagttaa ccagttttat accaaaaaat gcatgtttga ggaattgtct1620  
gaaattggga caaaacacct tcatgtaaac cagctttgca aaattttcca gcccagatac1680  
tcttcatcta ttcaaatgga ttgtcttatt ctgagcaaaag acctgttgtt aatcttcaag1740  
ctaggttttg cagttcccaa ccacaacatt ctctattttt gccaggctgg tgcaaaagta1800  
ttaaagatgt caatcagaaa tgtcaatgag actaaagtgg ttttgtaaat ctacgtata1860  
tttagcaaca ctccatgtag ctaatatatt ttggtagcat ctggtagacc ttagaatgtt1920  
acatagccag taggttcttt attcaaattt taagtatctt aagaatagta gggcagtaac1980  
agttactttt gagagttttc tgggtcaagct tttaccaggc attctctagc cttgggtacaa2040  
aaaaaaaaaa aacctgctgg ttgctgcagat acctaggctt gtccatttta tgcatttcag2100  
caaagtcatt ggatactatt gcaacttggg aatactggct tgcacaaagt ttattcggta2160  
gtttgaccgc tagtatgttg gaagttattt ggattgtttt tgggaattttg actggctgaa2220  
ttatgggttg tataaagtta tgtgtataac tggcaggctt atttatctgt tgcacttggg2280  
tagctttaat tgttctgtat tatttaaaaga taagtttact caacaataaa tctgcagaga2340  
ttgaacaaat aaaaaaaaaa aaaaaaa 2367

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## (2) INFORMATION ON SEQ ID NO. 8:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 568 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

ctcgagccgt gggcagtgcc cgcgaatgcg cggagacact gaccttcagc gcctcggctc 60
cagcgccatg gcgccctcca ggaagttctt cgttggggga aactggaaga tgaacggggc 120
gaagcagagt ctggggggagc tcatcggcac tctgaacgcg gccaaagggtgc cggccgacac 180
cgaggtggtt tgtgctcccc ctactgccta tctgacttc gcccggcaga agctagatcc 240
caagattgct gtggctgctc agaactgcta caaagtgact aatggggctt ttactgggga 300
gatcagccct ggcattgatca aagactgctg agccacgtgg gtggtcctgg ggcactcaga 360
gagaaggcat gtctttgggg agtcagatga gctgattggg cagaaagtgg cccatgctct 420
ggcagagggg ctgggagtaa tcgcctgcat tggggagaaag ctatgatgaa ggggaagctg 480
catcactgag aatggtgttt tcgagcagac aaaggctcatc ggggatgact tgaaggactg 540
gatcaagttc gtcctggcct gttggcct

```

568

## (2) INFORMATION ON SEQ ID NO. 9:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1775 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

00673400.122700

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ctcggggggcc attttgtgaa gagacgaaga ctgagcggtt gtggccgcgt tgccgacctc 60  
 cagcagcagt cggcttctct acgcagaacc cgggagtagg agactcagaa tcgaatctct 120  
 tctccctccc cttcttgtga gatttttttg atcttcagct acattttcgg ctttgtgaga 180  
 aaccttacca tcaaacacga tggccagcaa cgttaccaac aagacagatc ctcgctccat 240  
 gaactcccgt gtattcattg ggaatctcaa cactcttggt gtcaagaaat ctgatgtgga 300  
 ggcaatcttt tcgaagtatg gcaaaattgt gggctgctct gttcataagg gctttgcctt 360  
 cggtcagtat gttaatgaga gaaatgcccg ggctgctgta gcaggagagg atggcagaat 420  
 gattgctggc cagggttttag atattaacct ggctgcagag ccaaaagtga accgaggaat 480  
 agcaggtgtg aaacgatctg cagcggagat gtacggctcc tcttttgact tggactatga 540  
 ctttcaacgg gactattatg ataggatgta cagttacca gcacgtgtac ctctctctcc 600  
 tcctattgct cgggctgtag tgccctcgaa acgtcagcgt gtatcaggaa acacttcacg 660  
 aaggggcaaa agtggcttca attctaagag tggacagcgg ggatcttcca agtctggaaa 720  
 gttgaaaagg gatgacctc aggccattaa gaaggagctg acccagataa aacaaaaagt 780  
 ggattctctc ctggaaaacc tggaaaaaat tgaaaaaggaa cagagcaaac aagcagtaga 840  
 gatgaagaat gataagtcag aagaggagca gagcagcagc tccgtgaaga aagatgagac 900  
 taatgtgaag atggagtctg aggggggtgc agatgactct gctgaggagg gggacctact 960  
 ggatgatgat gataatgaag atcgggggga tgaccagctg gagttgatca aggatgatga 1020  
 aaaagaggct gaggaaggag aggatgacag agacagcgcc aatggcgagg atgactctta 1080  
 agcacatagt ggggttttag aatcttatcc cattatttct ttacctaggc gcttgtctaa 1140  
 gatcaaatgt ttcaccagat cctctcccct agtatcttca gcacatgctc actgttctcc 1200  
 ccctccttgt ccttcccatg ttcatttaatt catattgccc cgcgcctagt cccattttca 1260  
 cttcctttga cgctcctagt agttttgtta agtcttacc tgtaattttt gcttttaatt 1320  
 ttgatacctc tttatgactt aacaataaaa aggatgtatg gtttttatca actgtctcca 1380  
 aaataatctc ttgttatgca gggagtacag ttcttttcat tcatacataa gttcagtagt 1440  
 tgcttcccta actgcaaagg caatctcatt tagttgagta gctcttgaaa gcagctttga 1500  
 gttagaagta tgtgtgttac accctcacat tagtgtgctg tgtggggcag ttcaacacaa 1560  
 atgtaacaat gtatttttgt gaatgagagt tggcatgtca aatgcatact ctagaaaaat 1620  
 aattagtgtt atagtcttaa gatttgtttt cttaaagttga tactgtgggt tatttttgtg 1680  
 aacagcctga tgtttgggac ctttttctct caaaataaac aagtccttat taaaccagga 1740  
 atttggagaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1775

## (2) INFORMATION ON SEQ ID NO. 10:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 509 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

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(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
caggctcgagt ggccactgcg cagaccagac ttcgctcgta ctgctgcgcc tcgcttcgct 60
tttcctccgc aaccatgtct gacaaaccg atatggctga gatcgagaaa ttcgataagt120
cgaaactgaa gaagacagag acgcaagaga aaaatccact gccttccaaa gaaacgattg180
aacaggagaa gcaagcaggc gaatcgtaat gaggcgtgcy ccgccaatat gcactgtaca240
ttccacaagc attgccttct tattttactt cttttagctg ttttaactttg taagatgcaa300
agaggttgga tcaagtttaa atgactgtgc tgcccctttc acatcaaagg gactacttga360
acaacggaag ggccgcggcc tacctttccc atctgtctat ctatctggct ggcagggaag420
ggaagagttg cagggttggtg aggaagaagt ggggtggaag aagttggatg ggccgccagt480
aaaacttggg taaaccgaac ttggccaag 509
```

(2) INFORMATION ON SEQ ID NO. 11:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 2191 base pairs  
(B) TYPE: Nucleic acid  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:  
(A) ORGANISM: HUMAN  
(C) ORGAN:

(vii) OTHER ORIGIN:  
(A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

actgagcgaq ggccagccgt gcggcatcta caccgagcgc tgtggctccg gccttcgctg 60  
 ccagccgtcg cccgacgagg cgcgaccgct gcaggcgctg ctggacggcc gcgggctctg 120  
 cgtcaacgct agtgccgtca gccgcctgcg cgcctacctg ctgccagcgc gccagctcc 180  
 aggaaatgct agtgagtcgg aggaagaccg cagcgcgggc agtgtggaga gccctccgt 240  
 ctccagcacg caccgggtgt ctgatcccaa gtccaccccc ctccattcaa agataatcat 300  
 catcaagaaa gggtatgcta aagacagcca gcgtacaaa gttgactacg agtctcagag 360  
 cacagatacc cagaacttct cctccgagtc caagcgggag acagaatatg gtccctgccg 420  
 tagagaaatg gaagacacac tgaatcacct gaagttcctc aatgtgctga gtcccagggg 480  
 tgtacacatt cccaactgtg acaagaaggg attttataag aaaaagcagt gtcgcccttc 540  
 caaaggcagg aagcggggct tctgctgggtg tgtggataag tatgggcagc ctctcccagg 600  
 ctacaccacc aagggggaagg aggacgtgca ctgctacagc atgcagagca agtagacgcc 660  
 tgccgcaagg ttaatgtgga gctcaaatat gccttatttt gcacaaaaga ctgccaaagg 720  
 catgaccagc agctggctac agcctcgatt tatatttctg tttgtggtga actgattttt 780  
 tttaaaccaa agtttagaaa gaggtttttg aaatgcctat ggtttctttg aatggtaaac 840  
 ttgagcatct tttcactttc cagtagtcag caaagagcag tttgaatttt ctgtgcgctt 900  
 cctatcaaaa tattcagaga ctcgagcaca gcacccagac ttcatgcgcc cgtggaatgc 960  
 tcaccacatg ttggtcgagg cggccgacca ctgactttgt gacttagggc gctgtgttc 1020  
 ctatgtagag aacacgcttc acccccactc cccgtacagt gcgcacaggc tttatcgagal 1080  
 ataggaaaaac ctttaaacc cggtcacccg gacatcccaa cgcatgctcc tggagctcac 1140  
 agccttctgt ggtgtcattt ctgaaacaag ggcgtggatc cctcaaccaa gaagaatgtt 1200  
 tatgtcttca agtgacctgt actgcttggg gactattgga gaaaataagg tggagtccta 1260  
 cttgtttaaa aaatatgtat ctaagaatgt tctagggcac tctgggaacc tataaaggca 1320  
 ggtatttctg gccctcctct tcaggaatct tcctgaagac atggcccagt cgaaggccca 1380  
 ggatggcttt tgctgcggcc ccgtggggta ggagggacag agagacaggg agagtcagcc 1440  
 tccacattca gaggcattac aagtaatggc acaattcttc ggatgactgc agaaaatagt 1500  
 gttttgtagt tcaacaactc aagacgaagc ttatttctga ggataagctc tttaaaggca 1560  
  
 aagctttatt ttcattcttc atcttttgtc ctcttagca caatgtaaaa aagaatagta 1620  
 atatcagaac aggaaggagg aatggcttgc tggggagccc atccaggaca ctgggagcac 1680  
 atagagattc acccatgttt gttgaactta gagtattctt catgtttttc tttataattc 1740  
 acacatatat gcagagaaga tatgttcttg ttaacattgt atacaacata gcccacaaata 1800  
 tagtaagatc tatactagat aatcctagat gaaatgttag agatgctata tgatacaact 1860  
 gtggccatga ctgaggaaa gaggctcacgc ccagagactg ggctgctctc ccggaggcca 1920  
 aacccaagaa ggtctggcaa agtcaggctc agggagactc tgccctgctg cagacctcgg 1980  
 tgtggacaca cgctgcatag agctctcctt gaaaacagag gggctcgaag acattctgcc 2040  
 tacctattag cttttcttta tttttttaac tttttggggg gaaaagtatt tttgagaagt 2100  
 ttgtcttgca atgtatttat aaatagtaaa taaagttttt accattaaaa aaaaaaggag 2160  
 taaaaagaaa aaaaaggggc gccgccgact a 2191

002221 00432960

## (2) INFORMATION ON SEQ ID NO. 12:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1769 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

attattttaca tttcaaaaata attccccctta atcgtttttac tcctaagttc attaccattg 60
ttggcccacc ttaggttcca ccacttggtt gttaccccag ccctgggttc aaacagggac 120
atggcaaggg gacacaggac agaggggtcc ccagctgcc cctcaccac cgcaattcat 180
ttagtagcag gcacaggggc agctccggca cggctttctc aggcctatgc cggagcctcg 240
agggctggag agcgggaaga caggcagtgc tcggggagtt gcagcaggac gtcaccagga 300
ggcggaacgg ccacgggagg gggggcccgc gacattgcgc agcaaggagg ctgcaggggc 360
tcggcctgcg ggcgcccgtc ccacgaggca ctgcggccca gggctctggtg cggagagggc 420
ccacaagtga cttggtgacg ctgtatgccc tcaccgctca gcccctgggg ctggcttggc 480
agacagtaca gcatccaggg gagtcaaggg catggggcga gaccagacta ggcgagggcg 540
gcggggcgga gtgaatgagc tctcaggagg gaggatggtg caggcagggg tgaggagcgc 600
agggggcggc gagcgggagg cactggcctc cagagcccgt ggccaaggcg ggcctcgcg 660
gcggcgacgg agccgggatc ggtgcctcag cgttcgggct ggagacgagg ccaggtctcc 720
agctggggtg gacgtgcccc ccagctgccc aaggcaagac gccaggtccg gtggacgtga 780
caagcaggac atgacatggt ccggtgtgac ggcgaggaca gaggaggcgc gtccggcctt 840
cctgaacacc ttaggctggt ggggctgcgg caagaagcgg gtctgtttct ttacttcctc 900
cacggagtcg gcacactatg gctgccctct gggctcccag aaccacaaac atgaaagaaa 960
tggtgctacc cagctcaagc ctgggccttt gaatccggac aaaaaaccct ctagcttggaa 1020
aatgaatatg ctgcacttta caaccactgc actaactgac taaggaatcg gctctggaag 1080
gtgaaqctag aggaaccaga cctcatcagc ccaacatcaa agacaccatc ggaacagcag 1140
cgcccgcagc acccaccctc caccggcgac tccatcttca tggccacccc ctgcggcgga 1200

cggttgacca ccagccacca catcatccca gagctgagct cctccagcgg gatgacgccg 1260
tccccaccac ctccctcttc ttctttttca tccttctgtc tctttgtttc tgagctttcc 1320
tgtctttcct tttttctgag agattcaaa cctccacgac tctgtttccc ccgtcccttc 1380
tgaatttaat ttgcactaag tcattttgac tgggttgagt tgtggagacg gctttgagtc 1440
tcagtacgag tgtgcgtgag tgtgagccac cttggcaagt gcctgtgcag gggccggccg 1500
ccctccatct gggccgggtg actgggcgcc ggctgtgtgc ccgaggcctc accctgccct 1560
cgccctagtc ggaagctccg accgacatca cggagcagcc ttcaagcatt ccattacgcc 1620
ccatctcgct ctgtgcccc cccaccaggg gcttcagcag gagccctgga ctcatcatca 1680
ataaacactg ttacagcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaag

```

1769

09673400.122700

## (2) INFORMATION ON SEQ ID NO. 13:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

aaaagctgtc cgcgcgggga gccagggcc agctttgggg ttgtccctgg acttgtcttg 60
gttccagaac ctgacgaccc ggcgacggcg acgtctcttt tgactaaaag acagtgtcca 120
gtgctccagc ctaggagtct acggggaccg cctcccgcgc cgccaccatg cccaacttct 180
ctggcaactg gaaaatcatc cgatcggaaa acttcgagga attgctcaaa gtgctggggg 240
tgaatgtgat gctgaggaag attgctgtgg ctgcagcgtc caagccagca gtggagatca 300
aacaggaggg agacactttc tacatcaaaa cctccaccac cgtgcgcacc acagagatta 360
acttcaagggt tggggaggag tttgaggagc agactgtgga tgggaggccc tgtaagagcc 420
tggtgaaatg ggagagttag aataaaatgg tctgtgagca gaagctcctg aagggagagg 480
gccccaaagc ctctgtggacc agagaactga ccaacgatgg ggaactgac ctgaccatga 540
cggcggatga cgttgtgtgc accagggtct acgtccgaga gtgagtggcc acaggtagaa 600
ccgcggccga agcccaccac tggccatgct caccgcctg ctctactgcc cctccgtcc 660
caccctctcc ttctaggata gcgtctccct taccctcagtc acttctgggg gtctactggg 720
tgctctttgc aggttcttgc tttctttgac ctctctcttc ctccctaca ccaacaaaga 780
ggaatggctg caagagccca gatcaccat tccgggttca ctcccgctt ccccaagtca 840
gcagtcctag ccccaaacca gccagagca gggctctctt aaaggggact tgagggcctg 900
agcaggaaaag actggccctc tagctctac cctttgtccc tgtagcttat acagtttaga 960
atatttattt gttaatttta ttaaaatgct ttaaaaaaat aaaaaaaaaa aaaaaaaaaa 1020
aaaaaa                                     1026

```

## (2) INFORMATION ON SEQ ID NO. 14:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 676 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

09673400.122700

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

```

ggccattttg tgaagagacg aagactgagc ggttggtggcc gcggtgcccga cctccagcag 60
cagtcgggctt ctctacgcag aaccggggag taggagactc agaatcgaat ctcttctccc120
tcccccttctt gggcagcaag gcgaacccca tccctactca ctggagctca gctttgattt180
ttaacctccc tccccacccc ttccagaaca cacacattcc attccaaaac tgattttata240
aagacatttt aaacataatg atgcaacttg gtgtgcaacta cagcaaatgt acaggtgttt300
tttttttaat tgtttccaaa accggggacct ggatttaaga tgtaattttt aaaatttcta360
tttctatttt ttgggcagca gttgggttag agggaggagga gccttttagc ctcccagaaa420
ctgacctctc tacttctctg tgtattttta agattgattg atgatgtgga aagggccttg480
cttgctctgct actgaaaact ttatccttgc ggtttttgtg gaactgcgtt tggaaaagaga540
aaagaaatga actttactga cttgacattt tgcacctccc ggtttttcgaa tctgggcaat600
tttaattttg gttttacagt gagagttttt gatctcagca cagaagtaat ccaatttttt660
ttagcatttt ccgact                                     676

```

(2) INFORMATION ON SEQ ID NO. 15:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1254 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

00673400.122700



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

cggctcgagc agctcgagcg gctcaaacac ctcatttgac cttgccagct gaccttcaaa 60  
 cccctgcattt gaaccgacca acatttaagtc cagagagtaa acttgaatgg aataacgaca 120  
 ttccagaagt taatcatttg aattctgaac actggagaaa aaccgaaaaa tggacggggc 180  
 atgaagagac taatcatctg gaaaccgatt tcagtggcga tggcatgaca gagctagagc 240  
 tcgggccccag ccccaggctg cagcccattc gcaggcaccg gaaagaactt cccagtatg 300  
 gtggtcctgg aaaggacatt tttgaagatc aactatatct tcctgtgcat tccgatggaa 360  
 tttcagttca tcagatgttc accatggcca ccgcagaaca ccgaagtaat tccagcatag 420  
 cgggggaagat gttgaccaag gtggagaaga atcacgaaaa ggagaagtca cagcacctag 480  
 aaggcagcgc ctccctcttca ctctcctctg attagatgaa actgttacct taccctaaac 540  
 acagtatctt tttttaacct ttttatttgt aaactaataa aggtaatcac agccaccaac 600  
 attccaagct accctgggtg cctttgtgca gtagaagcta gtgagcatgt gagcaagcgg 660  
 tgtgcacacg gagactcatc gttataatct actatctgcc aagagtagaa agaaaggctg 720  
 gggatatattg ggttggtctg gttttgattt tttgcttggt tgtttgtttt gtactaaaac 780  
 agtattatct tttgaatata gtaggacatc aagtatatat atgttatcca atcaagatgg 840  
 ctagaatggg gcctttctga gtgtctaaaa cttgacaccc ctggtaaatc tttcaacaca 900  
 cttccactgc ctgcgtaatg aagttttgat tcatttttaa ccactggaat ttttcaatgc 960  
 cgtcattttc agttagatga ttttgcactt tgagattaaa atgccatgtc tatttgattal 1020  
 gtcttatttt tttattttta caggcttata agtctcactg ttggctgtca ttgtgacaaa 1080  
 gtcaataaaa cccccaagga cgacacacag tatggatcac atattgtttg acattaagct 1140  
 tttgccagaa aatgtttgat gtgttttacc tcgacttgct aaaatcgatt agcagaaaagg 1200  
 catggctaata aatgtttggtg gtgaaaataa ataaataagt aaacaaaaag aaaa 1254

## (2) INFORMATION ON SEQ ID NO. 16:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 537 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09673400-122700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

```

ggccccggggcc cccaccctcg acatgcgctt ccggcgacgc cttagcgctg acccccacgc 60
aaccacagcga aactccgcgg aggcgcgcgg cactgatggac ggtcgggtgc agctgatgaal20
ggccctcctg gccgggcccc tccggccccg ggcgcgtcgc tggaggaacc cgattccctt180
tcccagagacg tttagcggag ataccgaccg actcccggag ttcacgtcgc agacgtgctc240
ctacatgttc gtggacgaga acacgtttct caacgacgcc ctgaagggtga cgttcctcat300
caccgcctc acggggccag ccctgcagtg ggtgatcccc tacatcagga aggagagccc360
cctgctcaat gattaccggg gctttctggc cgagatgaag cgagtctttg gatgggagga420
ggacgaggac ttctaggccg ggagaccctc gggcctgggg gcgggtgctc tgggaagagt480
tcgctgtgcc agtggccacc gctagggtct ccacaggcgc cctcccagc gaatgct 537

```

## (2) INFORMATION ON SEQ ID NO. 17:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 823 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

tagactgaac aggaggggga gtcctgggta gcgcgcgggt ctaaatcggt acttggcgga 60
aagttcccat gagtctttgc cagcgtcccc ctccctttgt gaggattggg atattccgac120
tccttaaggg cctggcgcac ataagggtgt accttttcat tcccgttgtt atggagggcc180
acatctgcca gagcctggag tctgcgaagg ccgggacccg gttccccggc ccacagtggg240
ggtgtgcaaa cccgagagaa ctgggttgca aattcgtgaa gaatcagcat catgtttggc300
agctgagtat tggagccagg agcctgccat gaggttttga gaacagagt ctgttttaga360
gctggcagca gcatctcagc ccaagagaag gttatatcc cagaggatgt cagtcccaag420
gaccagtagc tgccatcagt ttggattctg aaaactaact ggcataca ca ctgggtgtag480
aaacatgctt gccttatgta tcagaggaca tgctcagcag atccaagaga tatatttggc540
aactttttct agaaaaggca cattgggtat cattcattac attcttgagg ttttttggg600
tttttttttt ttttttttga gacagtcttg ctgtattgcc caggctggga gtgtgggtggc660
acaatcacag ctcatgcat cctcaatcac ccagggccta agcaatcctc ccaccttgta720
gctgggacta cagctcacag cacaccgggc taaaattttt tttgttgag acggtttttc780
tatgttgccc ggggtggtttt cagggtccgg ggttcagatg gtc 823

```

09673400-122700

## (2) INFORMATION ON SEQ ID NO. 18:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

gggcgcacat aaggtgtgac cttttcattc ccgttggtat ggagggccac atctgccaga 60
gcctggagtc tgcgaaggcc gggacccggt tccccggccc acagtggggg tgtgcaaacc 120
cgagagaact ggtcgtgtaa acctctacaa cttagttgac cgtaactgcc agagccctgc 180
cctgaattcc tgtccttact cctctcttaa gattgcgtac ccactgcaga gtgctgaaga 240
cggggtagcc acgaggttgc aaattcgtga agaatcagca tcatgtttgg cagctgagta 300
ttggagccag gagcctgcca tgaggttttg agaacagagt gctgttttag agctggcagc 360
agcatctcag cccaagagaa ggttatattc ccagaggatg tcagtcccaa ggaccagtag 420
ctgccatcag tttggattct gaaaactaac tggcatcaac actgggtgta gaaacatgct 480
tgccttatgt atcagaggac atgctcagca gatccaagag atatatattg caactttttc 540
tagaaaaggc acattgggta tcattcatta cattcttgag tttttttggg tttttttttt 600
ttttttttga gacagtcttg ctgtattgcc caggctggag tgtggtggca caatcacagc 660
tcattgcatc ctcaatcacc caggcctaag caatcctccc acctgttagc tgggactaca 720
gctcacagca cacctggcta aaattttttt tttgttgaga cggattctct atgttgccca 780
ggctggtctc aggtctctgg gctcagatgg tcctcctgcc tcagcttcca aaggcacagg 840
ccaagttgta gctttgtccc ttgccatcat gcccaacaag aggttctata ctttttaatg 900
aattgacttt cataaattgg ttatgttggg gggcaagttc ttttaagctg aaattgtaaa 960
ttcctcctga aatgtttttt catgcagtta ccatgaacta atactacaat aaaggatggt 1020
cttgggtgtc aaaaaaaaaa aaaaaaaaaa aaaaagaaaa aaaaaaaaaa aaaaaaaaaa 1080
aa

```

## (2) INFORMATION ON SEQ ID NO. 19:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1548 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

002221 004E2960

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

ccccattccat aggggaatgag ctgggctgtc ctttctcccc acgttcacct gcacttcgtt 60
agagagcagt gttcacatgc cacaccacaa gatccccaca atgacataac tccattcaga 120
gactggcgtg actgggctgg gtctccccac ccccccttc agctcttgta tcaactcaga 180
tctggcagcc agttccgtcc tgacagagtt cacagcatat attggtggat tcttgtccat 240
agtgcattctg ctttaagaat taacgaaagc agtgtaaga cagtaaggat tcaaaccatt 300
tgccaaaaat gagtctaagt gcatttactc tcttccctggc attgattggg ggtaccagtg 360
gccagtacta tgattatgat tttcccttat caatttatgg gcaatcatca ccaaactgtg 420
caccagaatg taactgccct gaaagctacc caagtgccat gtactgtgat gagctgaaat 480
tgaaaagtgt accaatggtg cctcctggaa tcagtatct ttaccttagg aataaccaga 540
ttgaccatat tgatgaaaag gcctttgaga atgtaactga tctgcagtgg ctcttctag 600
atcacaacct tctagaaaac tccaagataa aaggggagag tttctctaaa ttgaaacaac 660
tgaagaagct gcatataaac cacaacaacc tgacagagtc tgtgggcccc cttcccaaat 720
ctctggagga tctgcagctt actcataaca agatcacaaa gctgggctct tttgaaggat 780
tggtaaacct gaccttcata catctccagc acaatcggct gaaagaggat gctgtttcag 840
ctgcttttaa aggtctttaa tcaactgaat accttgactt gagcttcaat cagatagcca 900
gactgccttc tggctctcct gtctctcttc taactctcta cttagacaac aataagatca 960
gcaacatccc tgatgagtat ttcaagcgtt ttaatgcatt gcagtatctg cgtttatctc 1020
acaacgaact ggtgatagt ggaatacctg gaaattcttt caatgtgtca tccctgggtg 1080
agctggatct gtccataaac aagcttaaaa acataccaac tgtcaatgaa aaccttgaaa 1140
actattacct ggaggtcaat caacttgaga agtttgacat aaagagcttc tgcaagatcc 1200
tgggggccatt atcctactcc aagatcaagc atttgcggtt ggatggcaat cgcattctcag 1260
aaaccagtct tccaccggat atgtatgaat gtctacgtgt tgctaacgaa gtcactcttal 1320
attaatatct gtatcctgga acaatatctt atggttatgt tttctctgtg gtcagttttc 1380
atagtatcca tattttatta ctgtttatta cttccatgaa ttttaaaatc tgagggaaat 1440
gttttgtaaa cttttatttt tttttaaagg aaaaggatgg aaaggccagg gcctaatttc 1500
catccaccaa ggaacacacc acattattcc acggaatagg ccattcggg 1548

```

(2) INFORMATION ON SEQ ID NO. 20:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 844 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

09673400.12300

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

acctgcagag ggggtccatac ggcgttggttc tggattcccg tcgtaactta aagggaaatt 60
ttcacaaatgt cgggagccct tcatgtcctg caaatgaagg aggaggatgt ccttaagttc120
cttgcagcag gaacccactt aggtggcacc aatcttgact tccagatgga acagtacatc180
tataaaagga aaagtgatgg catctatata ataaatctca agaggacctg ggagaagctt240
ctgctggcag ctgctgcaat tgttgccatt gaaaaccctg ctgatgtcag tgttatatcc300
tccaggaata ctggccagag ggctgtgctg aagtttgctg ctgccactgg agccactcca360
attgctggcc gcttcaactc tggaaacctc actaaccaga tccaggcagc cttccgggag420
ccacggcttc ttgtggttac tgacccacag gctgaccacc agcctctcac ggaggcatct480
tatgttaacc tacctaccat tgcgctgtgt aacacagatt ctctctgctg ctatgtggac540
attgcaatcc catgcaacaa caaggtaatg attttaggat cttagagttt tgaatgcgtg600
ctctagaaaa aacattcctg tgcacattgt tagagcttgg agttgaggct actgactggc660
cgatgaacte gcaagtgtag gtatgtgtgt acatgagggg caagttttcg ctaacaccac720
aagggctctt ggcccaatga gtggagtttg atagtaattc ttgctacaag tataacatta780
ctgcatgaca gctttgtgga gaaatgaaaa catttggaat atagtgtgtt ctctgccttg840
tcca

```

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 862 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

09673400.1E2700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

gagcaagaga gaaggaggcc cagacagtga gggcaggagg gagagaagag acgcagaagg 60  
 agagcgagcg agagagaaaag ggttctggat tggggggggag agcaaggagg ggaggaaggc120  
 ggtgagagag gcggggggcct cgggagggtg aaagggggga ggagaagggc ggggcacgga180  
 ggcccgaagc agggacaaga ctccgactcc agctctgact ttttccgagg ctctcggtt240  
 ccactgcagc catgtcactc ctcttgctgg tgggtctcagc ccttcacatc ctcatctta300  
 tactgctttt cgtggccact ttggacaagt cctgggtggac tctccctggg aaagagtccc360  
 tgaatctctg gtacgactgc acgtggaaca acgacaccaa aacatggggc tgcagtaatg420  
 tcagcgagaa tggctggctg aaggcgggtg aggtcctcat ggtgctctcc ctcatctct480  
 gctgtctctc ctccatcctg ttcatgttcc agctctacac catgcgacga ggaggtctct540  
 tctatgccac cggcctctgc cagctttgca ccagcgtggc ggtgtttact ggcgccttga600  
  
 tctatgccat tcacgcccag gagatcctgg agaagcacc cgcagggggc agcttcggat660  
 actgcttcgc cctggcctgg gtggccttcc ccttcgccc tggcagcggc atcatctaca720  
 tccacctacg gaagcgggag tgagcgcccc gcttcgctcg gctgcccccg ccccttccc780  
 gccccctcg ccgcgcgtcc tccaaaaaat aaaaccttaa ccgcggggaa aaaaaaaaa840  
 aaaaagggaag gaaaaaaaa aa 862

## (2) INFORMATION ON SEQ ID NO. 22:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 546 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

cccagccaag ggtccttcag gtaggaggtc ctgggtgact ttggaagtcc gtagtgtctc 60  
 attgcagata attttttagct tagggcctgg tggctagggtc ggttctctcc tttccagtcg120  
 gagacctctg ccgcaaacat gctccgccag atcatcgggtc aggccaaaga gcatccgagc180  
 ttgatccccc tctttgtatt tattggaact ggagctactg gagcaacact gtatctcttg240  
 cgtctggcat tgttcaatcc agatgtttgt tgggacagaa ataaccaga gccctggaac300  
 aaactgggtc ccaatgatca atacaagttc tactcagtga atgtggatta cagcaagctg360  
 aagaagggaac gtccagatct ctaaatgaaa tgtttcacta taacgctgct ttagaatgaa420  
 ggtcttccag aagccacatc cgcacaattt tccacttaac caggaaatat ttctcctctt480  
 aaatgaatga aatcaatggg ggggggcgct attggaagcc ctattggggg tcaagtgttg540  
 aataaa

546

09673400.122700

## (2) INFORMATION ON SEQ ID NO. 23:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1591 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```

gccgaggagc cgagcccgcc accccccgcg ccgcccgcgc cgcgccatggg ctgcctcggg 60
aacagtaaga ccgaggacca gcgcaacgag gagaaggcgc aggtgaggcc aacaaaaaga 120
tcgagaagca gctgcagaag gacaagcagg tctaccgggc cacgcaccgc ctgctgctgc 180
tgggtgctgg agaattctgtt aaaagcacca ttgtgaagca gatgaggatc ctgcatgtta 240
atgggtttta tggagacagt gagaaggcaa ccaaagtgca ggacatcaaa aacaacctga 300
aagaggcgat tgaaaccatt gtggccgcca tgagcaacct ggtgcccccc gtggagctgg 360
ccaaccccgga gaaccagttc agagtggact acattctgag tgtgatgaac gtgcctgact 420
ttgacttccc tcccgaaattc tatgagcatg ccaaggctct gtgggaggat gaaggagtgc 480
gtgcctgcta cgaacgctcc aacgagtacc agctgattga ctgtgcccag tacttccctg 540
acaagatcga cgtgatcaag caggctgact atgtgccgag cgatcaggac ctgcttcgct 600
gccgtgtcct gacttctgga atctttgaga ccaagttcca ggtggacaaa gtcaacttcc 660
acatgtttga cgtgggtggc cagcgcgatg aacgccgcaa gtggatccag tgcttcaacg 720
atgtgactgc catcatcttc gtggtggcca gcagcagcta caacatggtc atccgggagg 780
acaaccagac caaccgctg caggaggctc tgaacctctt caagagcatc tggaacaaca 840
gatggctgcg caccatctct gtgatcctgt tctcaacaa gcaagatctg ctgctgaga 900
aagtccttgc tgggaaatcg aagattgagg actactttcc agaatttgct cgctacacta 960
ctcctgagga tgctactccc gagccccgag aggacccacg cgtgacccgg gccaaagtact 1020
tcattcgaga tgagtttctg aggatcagca ctgccagtgg agatgggcgt cactactgct 1080
accctcattt cacctgcgct gtggacactg agaacatccg ccgtgtgttc aacgactgcc 1140
gtgacatcat tcagcgcagt caccttcgtc agtacgagct gctctaagaa gggaaccccc 1200
aaatttaatt aaagccttaa gcacaattaa ttaaaagtga aacgtaattg tacaagcagt 1260
taatcaccca ccatagggca tgattaacaa agcaaccttt ccttcccccc gagtgttttt 1320
gcgaaaacccc cttttccctt cagcttgctt agatgtttcc aatttagaaa gcttaaggcg 1380
gcctacagaa aaaggaaaaa aggccacaaa agttcccttc cactttcagt aaaaataaat 1440
aaaacagcag cagcaaacaa ataaaatgaa ataaaagaaa caaatgaaat aaatattgtg 1500
ttgtgcagca ttaaaaaaaa tcaaaaataa aattaaatgt gagcaaaagg aaaaaaaaaa 1560
ggcaaaaggg gaaagaagaa aagggggggg g

```

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## (2) INFORMATION ON SEQ ID NO. 24:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 441 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

```

ggcaggcaga tacgttcgtc agcttgctcc tttctgcccg tggacgccgc cgaagaagca 60
tcgttaaagt ctctcttcac cctgccgtca tgtctaagtc agagtctcct aaagagcccgl20
aacagctgag gaagctcttc attggagggt tgagctttga aacaactgat gagagcctga180
ggagccattt tgagcaatgg ggaacgctca cggactgtgt ggtaatgaga gatccaaaca240
ccaagcgctc caggggcttt gggtttgtca catatgccac tgtggaggag gtggatgcag300
ctatgaatgc aaggccacac aaggtggatg gaagagttgt ggaaccaaag agagctgttt360
cagagaagat ttgaaaagcc aggtgccact tacctgtgaa aaggtatttg ttggtggatt420
aaggagcact tgagacatca c

```

441

## (2) INFORMATION ON SEQ ID NO. 25:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1131 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

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(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

cgggaggtga aatccggttc taaccgggtcc ggggctccca ggcgtataaa aactttataa 60
accccccgga gcccagagcag tgtgaagaag aggcgagaac gacccccgga ccgaccaaag 120
cccgcgcgcc gctgcatccc gcgtccagca cctacgtccc gctgccgtcg ccgccgccac 180
catgccccaa agaaaggctg aaggggatgc taaggagat aaagcaaagg tgaaggacga 240
accacagaga agatccgcga ggttgtctgc taaacctgct cctccaaagc cagagcccaa 300
gcctaaaaag gccctgcaa agaagggaga gaaggtaccc aaagggaaaa agggaaaaagc 360
tgatgctggc aaggagggga ataaccctgc agaaaatgga gatgccaaaa cagaccaggc 420
acagaaaagc gaaggtgctg gagatgccaa gtgaagtgtg tgcatttttg ataactgtgt 480
acttctgggt actgtacagt ttgaaatact attttttatc aagttttata aaaatgcaga 540
attttgtttt actttttttt tttttttaa agctatgttg ttagcacaca gaacacttca 600
ttgttgtttt tgggggaagg ggcataatgc actaatagaa tgtctccaaa gctggattga 660
tgtggagaaa acacctttcc cttctagttt tgagagactt cctcttggtt cccaggagga 720

gggattccct gactttgaca cacatggcca ccttggcaca aaagccttgt ggtatagaaa 780
aacaaatttg tttttatgtc ctcttctccc ttccatctt tcagcataga cttactccc 840
ttaagcccag acatctgttg agacctgacc cctagtcatt ggttaccagt gtgtcaggca 900
atctggactt tccagtgatg ccactgagat ggcacctgtc aaaagagcag tggttccatt 960
tctagattgt ggatcttcag ataaattctg ccattttcat ttcacttccet gaaagtcagg 1020
gtcggcttgt gaaaagtgtt taaacaacat gctaaatgtg aaatgtcaac cctcactcta 1080
aaacttttcc ctgggtcaga ggatccgatg gaggacttca attgggggtt t 1131

```

(2) INFORMATION ON SEQ ID NO. 26:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gtaccctcaa agacagagac accaagaaga atcggaacat acaggctttg atatcaaagg 60
tttataaaagc caatatctgg gaaagagaaa accgtgagac ttccagatct tctctggtga 120
agtgttgttt cctgcaacga tcacgaacat gaacatcaaa ggatcgccat ggaaaggggtc 180
cctcctgctg ctgctggtgt caaacctgct cctgtgccag agcgtggccc ccttgcccat 240
ctgtcccggc ggggctgccc gatgccaggt gacccttcga gacctgtttg accgcgccgt 300
cgctcctgtcc cactacatcc ataacctctc ctcaaaaaatg ttccagcgaat tcgataaacg 360
gtatacccat ggcgggggtg tcattaccaa ggccatcaac agctgccaca cttcttccct 420
tgccaccccc gaagacaagg agcaagccca acagatgaat caaaaagact ttctgagcct 480
gatagtcagc atattgcgat cctggaatga gcctctgtat catctggtca cggaaagtacg 540
tggtatgcaa gaagccccgg aggcctatcct atccaaaagct gtagagattg aggagcaaac 600
caaacggctt cttagaggga tgagagctgt agtcagccag gtccatcctg aaaccaaaga 660
aaatgagatc taccctgtct ggtcgggact tccatccctg cagatggctg atgaagagtc 720
tcgcctttct gcttattata acctgctcca ctgcctacgc agggattcac ataaaaatcg 780
caattatctc aagctcctga agtgccgaat catccacaac aacaactgct aagcccacat 840
ccatttcac cttttctgag aaggtcctta atgatccgtt ccattgcaag cttcttttag 900
ttgtatctct tttgaatcca tgcttgggtg taacagggtct cctcttaaaa aataaaaaact 960
gactccttag agacatcaaa atctaaaaaa acttaatggg ccggggcgag tggctcatgg 1020
ctgtggtccc ggcacttttg gaggccgagg caggcggatc aggaggtcag g 1071

```

## (2) INFORMATION ON SEQ ID NO. 27:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 896 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

gtgaccggct cagaccgggt ctggagacaa aagggggcgc ggccggccgga gcgggacggg 60
cccggcgcgg gagggagcga agagcgcggg cagcgagcga gatgcagcac cgaggcttcc120
tcctcctcac cctcctcgcc ctgctggcgc tcacctccgc ggtcgccaaa aagaaagata180
aggtgaagaa gggcgggccc gggagcgagt gcgctgagt ggcttggggg ccctgcaccc240
ccagcagcaa ggattgcggc gtgggtttcc gcgagggcac ctgcggggcc cagacccagc300
gcatccggtg caggggtgcc tgcaactgga agaaggagt tggagccgac tgcaagtaca360
agtttgagaa ctgggggtgc tgtgatggg gcacaggcac caaagtccgc caaggcacc420
tgaagaaggc gcgctacaat gctcagtgc aggagaccat ccgctcacc aagccctgca480
cccccaagac caaagcaaa gccaagcca agaaaggaa gggaaaggac tagacgcca540
gcctggatgc caaggagccc ctggtgtcac atggggcctg gccacgccc tccctctccc600
aggcccgaga tgtgaccac cagtgccttc tgtctgctcg ttagctttaa tcaatcatgc660
cctgccttgt cctctcact cccagcccc acccctaagt gcccaagtg gggagggaca720
agggattctg ggaagcttga gcctcccca aagcaatgt agtcccagag cccgcttttg780
ttcttcccca caattccatt actaagaaac acatcaaata aactgacttt tccccccaa840
aaaaagctct tcttttttaa tataaaaaaa aaaaaaaaaa aaaaaaaa aagaaa 896

```

## (2) INFORMATION ON SEQ ID NO. 28:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1050 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

ttttcatttt tttttttttt ttttctcag ttcaagttaa atacaaacta caaaagatta 60
atgggttgct ctactaatat atcatacaaa ccagtagcct gccacaacg ccaactcagg 120
ccattcctac caaaggaaga aaggctgggc tctccacccc ctgtaggaaa ggcctgcctt 180
gtaagacacc acaattcggc tgaattctgaa gtcttgtgtt ttactaatgg aaaaaaaaaa 240
tacagaagag gttttgttct catggctgcc caccgcagcc tggcactaaa acagcccaqc 300
gtcacttctt gcttggagaa atattctttg ctcttttggg catcaggctt gatggtatca 360
ctgccagggt tccagccagc tgggcacact tccccatgtt tgtcagttaa ctggaaggcc 420
tgaactagtc tcaaaagtct atccacagag cggccaacag ggaggtcatt tacagtgatc 480
tgccgaagaa tacccttatc atcaatgata aaaaggcccc tgaacgagat gccttcatca 540
gcctttaaga ccccataatc ctgagcaatg gtgcgcttcg ggtctgatac caaaggaatg 600
ttcatgggtc ccagtcctcc ttgtttctta ggtgtattga cccatgctag atgacagaag 660
tgagaatcca cagaagcacc aatcacttgg cagttgagtt tcttaaattc ttctgcccta 720
tcaactgaaq caatgatctc cgtggggcac acaaagggtg agtcaagagg gtaaaagaaq 780
aacacaacat attttctttt gtagtcagac aggttgatat ctttaaactg accatctggc 840
ataacagctg tggctttgaa gttgggggca gggcgcccaa ttttagcatt tccatgaagc 900
atcttccctat cagcagtcct aacacaagtc gcagaaacta accaccgaca ccaggcaaga 960
acaagacgcg caagagctct ccggggcgct gcctttatag ccagtaggga tctcgccaca1020
gtcggaaacg acgggggtgc cggagtagga

```

1050

00/22T 004E2960

## (2) INFORMATION ON SEQ ID NO. 29:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 581 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

## (vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

caggcttcct tctggcaaca ggcgtgggtc acgctctcgc tcggtcttcc tgccgccatc 60  
 ttggttccgc gttccctgca caaaatgccc ggcgaacacc agaaaccgtc cctgctacag120  
 agcaggagtt gccgcagccc caggctgaga cagggtctgg aacagaatct gacagtgatg180  
 aatcagtacc agagcttgaa gaacaggatt ccacccaggc aaccacacaa caagcccagc240  
 tggcggcagc agctgaaatc gatgaagaac cagtcagtaa agcaaaacag agtcggagtg300  
 aaaagaaggc acggaaggct atgtccaaac tgggtcttcg gcaggttaca ggagttacta360

gagtcactat ccggaaatct aagaatatcc tctttgtcat cacaaaacca gttgtctaca420  
 agagccctgc ttcagatacg tacatagttt ttggggaagc cagatcgaag attatcccag480  
 caagcacaac tagcagctgc tgagaagtca agttcagggtg aactgtctca acgttcagga540  
 aacccccggc ttccactgta gagggggaggt aaggggaggg t 581

## (2) INFORMATION ON SEQ ID NO. 30:

## (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 264 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

- (A) ORGANISM: HUMAN

00673400.122700

## (C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```

gggactatgt tgtgagcctg cgaaagaagt ttgtgtgggg actgtgggca gtgaatgcgt 60
tgggaacaat atggaaaact gggagctgcc ctacgtttct cccaagtgt gactcacttt120
cggggtgtcc caaaagcctg attccagggc ctgctagccc gaccccggtg acgcctccac180
ccgcgcctgg ccccagcctt caccgcgat cgccgcctc cggggcacac cctccgccag240
aaaacagccg gcgggcggcg agac                                     264

```

## (2) INFORMATION ON SEQ ID NO. 31:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 111 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

## (vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

## (vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

```

cggcgaatca cttataaatg gcgccgaagc aggagcccga aggcataatt gcaggagggg 60
tgagcgaatg crgrgctrrc atgggcctct tacgttgatg aggcataagta t      111

```

## (2) INFORMATION ON SEQ ID NO. 32:

## (i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 76 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

PFCEETKTER LWPRCRPPAA VGFSTQNPVG GDSESNLFSL PFLGSKANPI PTHWSSALIF60  
NLPSPPFQNT HIPFQN 76

(2) INFORMATION ON SEQ ID NO. 33:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 72 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

SSFLFSFQTQ FHKNRKDKVF SSRQAKPFPH HQSILKIHEE VERSVSGRLK GSSSSNPTAA60  
EKIEIEILKI TS 72

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 70 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

KKLDYFCAEI KNSHCKTKIK IAQIRKPGGA KCQVSKVHFF SLSKRSSTKT ARIKFSVADK60  
QSPFHIINQS 70

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## (2) INFORMATION ON SEQ ID NO. 35:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 60 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

SSGPAPGCSP FAGTRKNFPS MVVLERTFLK INYIFLCIPM EFQFIRCSPW PPQNTVIP60

## (2) INFORMATION ON SEQ ID NO. 36:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 63 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ASGVHTETHR YNLLSAKSRK KGWGYLGWLG FDFLLVCLFC TKTVLSFEYR RDISIYMLSN60  
QDG 63

## (2) INFORMATION ON SEQ ID NO. 37:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 170 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

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(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

ARAARAAQTP HLTLPADLQT LHLNRPTLS ESKLEWNNDI PEVNHLNSEH WRKTEKWTGH 60  
EETNHLETDF SGDGMTELEL GPSRLQPIR RHPKELPQYG GPGKDIFEDQ LYLPVHSDGI120  
SVHQMFMTAT AEHRNSSIA GKMLTKVEKN HEKEKSQHLE GSASSSLSSD 170

(2) INFORMATION ON SEQ ID NO. 38:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 144 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

ARAPTLDLRF RRRLSADPHA TQRNSAEARG TMDGRVQLMK ALLAGPLRPA ARRWRNPIPF 60  
PETFDGDTDR LPEFIVQTCS YMEVDENTFS NDALKVTFLI TRLTGPALQW VIPYIRKESPI20  
LLNDYRGFLA EMKRVEGWEE DEDF 144

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 178 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

HSLGRAPVET LAVATGTANS SQSTRPQARG SPGLEVLVLL PSKDSLHLGQ KAPVIEQGA 60  
LLPDVGDHPL QGWPREAGDE ERHLOGVVG E RVLVHEHVGA RLHDELRESV GISVKRLGKG120  
NRVFPATRRG PEGPGQEGH QLHPTVHRAA RLRGVSLGCV GVSASASPEA HVEGGGPG 178

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## (2) INFORMATION ON SEQ ID NO. 40:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 89 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

KLTGINTGCR NMLALCIRGH AQIQEIYLA TFSRKGTGLI IHYLEVFLG FFFFFLRQSC60  
 CIAQAGSVVA QSQLIASSIT QGLSNPPTL 89

## (2) INFORMATION ON SEQ ID NO. 41:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 95 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

IVTWRKVPMS LCQRPPPEVR IGIFRLLKGL AHIRCDLFIP VVMEGHICOS LESAKAGTRF60  
 PGPQWGCANP RELGCKFVKN QHHVWQLSIG ARSLP 95

## (2) INFORMATION ON SEQ ID NO. 42:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 154 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

002227.004E2960

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CQLVFRIQTD GSYWSLGLTS SGNITFSWAE MLLPALKQHS VLKTSWQAPG SNTQLPNMML 60  
ILHEFATQFS RVCTPPLWAG EPGPGLRRLQ ALADVALHNN GNEKVTPYVR QALKESEYPN120  
PHKRRGTLAK THGNFPPSND LDRRATQDSP SCSV 154

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 79 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

LASTLGVEIC LPYVSEDMLS RSKRYIWQLF LEKAHWVSFI TFLSFFGFFF FFFETVLLYC60  
PGWSVVAQSQ LIASSITQA 79

(2) INFORMATION ON SEQ ID NO. 44:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 82 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

CQLVFRIQTD GSYWSLGLTS SGNITFSWAE MLLPALKQHS VLKTSWQAPG SNTQLPNMML60  
ILHEFATSWL PRLQHSVGT QS 82

00222T 004E2960

## (2) INFORMATION ON SEQ ID NO. 45:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 68 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

RGSKDRNSGQ GSGSYGQLSC RGFSQDQFSRV CTPPLWAGEP GPGLRRLQAL ADVALHNNGN60  
 EKVTPLYVR 68

## (2) INFORMATION ON SEQ ID NO. 46:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 87 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

DYVVSRLRKKF VWGLWAVNAL GTIWKTGSCP QFLPKLOSLS GCPKSLIPGP ASPTPVTPPP60  
 APGPSLHPRS PPSGAHPPE NSRRAAR 87

## (2) INFORMATION ON SEQ ID NO. 47:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 51 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

00222700 123700

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

QALESGFWDT PKVSPTWGET EGSSQFSILF PTHSLPTVPT QTSFAGSQHS P

51

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 20 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

RRITYKWRRS RSPKAKLQEG

20

(2) INFORMATION ON SEQ ID NO. 49:

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 36 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GESLINGAEA GARRLNCRRG ERMLCFHGPL TLMRQS

36

004227-004E2960

## (2) INFORMATION ON SEQ ID NO. 50:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 26 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

KHSIRSPLLQ FSLRAPASAP FISDSP

26

## (2) INFORMATION ON SEQ ID NO. 51:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 25 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

EAHESTAFAH PSCNLAFGLL LRRHL

25

## (2) INFORMATION ON SEQ ID NO. 52:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 3665 base pairs
  - (B) TYPE: Nucleic acid
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual  
ESTs by assembling and editing

002221 0042960

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

GGCCATTTTG TGAAGAGACG AAGACTGAGC GGTGTGGGCC GCGTTGCCGA CCTCCAGCAG 60  
 CAGTCGGGCTT CTCTACGCAG AACCCGGGAG TAGGAGACTC AGAAATCGAA TCTCTTCTCC 120  
 CTCCCCTTCT TGGGCAGCAA GCGGAACCCC ATCCCTACTC ACTGGAGCTC AGCTTTGATT 180  
 TTTAACCTCC CTTCGCCACC CTTCCAGAAC ACACACATTC CATTCCAAAA CTGATTTTAT 240  
 AAAGACATTT TAAACATAAT GATGCAACTT GGTGTGCACT ACAGCAAATG TACAGGTGTT 300  
 TTTTTTTTAA TTGTTTCCAA AACCGGGACC TGGATTTAAG ATGTAATTTT TAAAATTTCT 360  
 ATTTCTATTT TTTCTGCAGC AGTTGGGTTA GAGGAGGAGG AGCCTTTTAG CCTCTCATAA 420  
 ACTGACCTCT CTACTTCCTC GTGTATTTTT AAGATTGATT GATGATGTGG AAAGGGCTTT 480  
 GCTTGTCTGC TACTGAAAAC TTTATCCTGC GGTTTTTGTG GAAACTGCTT TTGGAAGAG 540  
 AAAAGAAATG AACTTTACTG ACTTGACATT TTTGCACCTC CCGTTTTTCT AATCTGGGCT 600  
 ATTTTTATTT TTGTTTTTTT ACAGTGAGAT TTTTTTGATC TTCAGCTTAC ATTTTCGGGC 660  
 TTTGTGAGGA AACCTTTACC CATCAAACAC GATGGCCAGC AACGTTACCA ACAAGACAGA 720  
 TCCTCGCTCC ATGAACCTCC GTGTATTCAT TGGGAATCTC AACACTCTTG TGGTCAAGAA 780  
 ATCTGATGTG GAGGCAATCT TTTCGAAGTA TGGCAAATTT GTGGGCTGCT CTGTTCAATA 840  
 GGGCTTTGCC TTCGTTTCACT ATGTTAATGA GAGAAATGCC CGGGCTGCTG TAGCAGGAGA 900  
 GGATGGCAGA ATGATTGCTG GCCAGGTTTT AGATATTAAC CTGGCTGCAG AGCCAAAAGT 960  
 GAACCGAGGA AAAGCAGGTG TGAAACGATC TGCAGCGGAG ATGTACGGCT CCTCTTTTGA1020  
 CTTGGACTAT GACTTTCAAC GGGACTATTA TGATAGGATG TACAGTTACC CAGCACGTGT1080  
 ACCTCCTCCT CCTCCTATTG CTCGGGCTGT AGTGCCCTCG AAACGTCAGC GTGTATCAGG1140  
 AAACACTTCA CGAAGGGGCA AAAGTGGCTT CAATTCTAAG AGTGGACAGC GGGGATCTTC1200  
 CAAGTCTGGA AAGTTGAAAG GAGATGACCT TCAGGCCATT AAGAAGGAGC TGACCCAGAT1260  
 AAAACAAAAA GTGGATTCTC TCCTGGAAAA CCTGGAAAAA ATTGAAAAGG AACAGAGCAA1320  
 ACAAGCAGTA GAGATGAAGA ATGATAAGTC AGAAGAGGAG CAGAGCAGCA GCTCCGTGAA1380  
 GAAAGATGAG ACTAATGTGA AGATGGAGTC TGAGGGGGGT GCAGATGACT CTGCTGAGGA1440  
 GGGGGACCTA CTGGATGATG ATGATAATGA AGATCGGGGG GATGACCAGC TGGAGTTGAT1500  
 CAAGGATGAT GAAAAAGAGG CTGAGGAAGG AGAGGATGAC AGAGACAAGG CCAATGGCGA1560  
 GGATGACTCT TAAGCACATA GTGGGGTTTA GAAATCTTAT CCCATTATTT CTTTACCTAG1620  
 GCGCTTGTCT AAGATCAAAT TTTTCACCAG ATCCTCTCCC CTAGTATCTT CAGCACATGC1680  
 TCACTGTTCT CCCCATCCTT GTCCTTCCCA TGTTTATTAA TTCATATTGC CCGGCGGCTA1740

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GTCCCATTTT CACTTCCTTT GACGCTCCTA GTAGTTTTGT TAAGTCTTAC CCTGTAATTT1800  
 TTGCTTTTAA TTTTGATACC TCTTTATGAC TTAACAATAA AAAGGATGTA TGCTTTTAT1860  
 CAACTGTCTC CAAAATAATC TCTTGTTATG CAGGGAGTAC AGTTCTTTTC ATTCATACAT1920  
 AAGTTTCAGTA GTTGCTTCCC TAACGTGCAA GGCAATCTCA TTTAGTTGAG TAGCTCTTGA1980  
 AAGCAGCTTT GAGTTAGAAG TATGTGTGTT ACACCCTCAC ATTAGTGTGC TGTGTGGGGC2040  
 AGTTCAACAC AAATGTAACA ATGTATTTTT GTGAATGAGA GTTGGCATGT CAAATGCATC2100  
 CTCTAGAAAA ATAATTAGTG TTATAGTCTT AAGATTTGTT TTCTAAAGTT GATACTGTGG2160  
 GTTATTTTTG TGAACAGCCT GATGTTTGGG ACCTTTTTTC CTCAAAATAA ACAAGTCCTT2220  
 ATTAACCAG GAATTTGGAG AAAAAAAAAA AAAAAAATTT TTTATTTTTG TATTTTATTA2280  
 TTGTTTACTT CAAACTTTGT TTTACAGCGT CCTCCACAAA ACCTCTAGAA TGCCTAGAT2340  
 ATATTTTTCT TGGAGTCATA ATCATGATGC ATACCAACAC AACACTACTC AAATTATATT2400  
 TCATTGAGAT GCATGTTGCA TTGAGGAGTC AACTTGACAT AGAGTGGAGA CTTTTTCAA2460  
 ATGGCTTTTA CATCCTAATG AAAGTTTGGG AAGTATATCC TCTCTGCCTT TTCATCAGTG2520  
 CTTTGTGGTC CAGCTGGCAC CCTTTCTGAG GTTTGTGTTT TGTGCTAAAT GGTTTTGTCC2580  
 TTAAATAGGA GAGGCTCAAA AACATCAAGA TTTCAGGAAA ATGGCGACAC TGGCATAATG2640  
 GAACCCCTT GCTTCTATTT TGTTCTTTTA ATTACTATTT ATAGCCCCAG TTACCTTCTG2700  
 AATTCTGAAG TGTATATACC TCCATGTTCC TGAAAACAAG AAAACTCTTA CTTCTGATA2760  
 TTCCATAGAC TGCCTTCCCA GGTGATTGAG AACATAGAGA ATGTTACACA TTTATTTTAC2820  
 TCTAAATGAT CTTTTACCCC TGTTAGCTAA TCTTTGTGTT TTCCTCAACT TTATTAATTA2880  
 CAGTGATTGC ATTTTATGCA TCCAGTTGTA AGATGAATAT ATTAAACAGC TACCAGTGTT2940  
 GGTGATACCT CATCCTTGAA AGGCTTAGTT CATTTGTGTT TTATACTTCA GTTTTTCCAG3000  
 CATAGCAGAA AATGCCGCTT ATAATTTTTG TGCACACAAA CCTTGGAATC CCCCTGTAAA3060  
 GTTGCTATGG TTTCATAGCA TGCGGCACTG GCCCCTTTTT CATCCCCTC ATTACAGGCA3120  
 AAACCCATGT CTTATTTATG AGGATTTTAT AGATCATTTT CTGTAACAGG TGACAAAAGC3180  
 AGAAAAGAA GAAGAGGCTG AAGTATGAAC TACCCTTGGA GCCCATATAC ATGATATAGG3240  
 CAATTTCTTT TGTATGTTAA TTCAGTCAAA AATACTACCC ACTTGATGTT TTCTAATCTG3300  
 ATGTGAGCTC ATGTTACACA GACTTTTAGT AAGTAACCCG TGA CTAGAAA ATAACTGGA3360  
 TGCTTAGGAG AGAGTGTGAG ATGTATAAGA TGCTAATAAA ACCTGTTTAA TATTATTGTT3420  
 AGCTGTAAGT TTTTGGGAAA TACTGAACAA ATTAGTCCAC AATCAAGTGT CTACTTTTCC3480  
 CTTCACTGTA GGGCCTCTCC CTGCACAGAG CAGTCTGTTT AGCTGTGAAC ACCACAATCT3540  
 GCAGATGTTT AAGTCCCTTA CATAAAATGG CATAGTATTT ATATGTAACC TATGCATATT3600  
 CTCCTGTATA TTTTAAATCA TCTCTACATT AAAATACCTG ATAAATCTA AATAAAAAAA3660  
 AAAAA 3665

(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 301 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GNLYPSNTMA SNVTNKTDFR SMNSRVEIGN LNTLVVKKSD VEAIFSKYK IVGCSVHKGF 60  
 AFVQYVNERN ARAAVAGEDG RMIAGQVLDI NLAAEPKVN GKAGVKRSAA EMYGSSFOLD120  
 YDFQRDYYDR MYSYPARVPP PPPIARAVVP SKRQRVSGNT SRRGKSGFNS KSGQRGSSKS180  
 GKLGDDDLQA IKKELTQIKQ KVDSLLENLE KIEKEQSKQA VEMKNDKSEE EQSSSVKKD240  
 STNVKMESEG GADDSAEEDG LLDDDDNEDR GDDQLELIKD DEKEAEEDG DRDKANGEDD300  
 S 301

09673400.122700

## (2) INFORMATION ON SEQ ID NO. 54:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 112 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

ESSSPLALSL SSSPSSASFS SSLINSSWSS PRSSLSSSSS RSPSSAESSA PPSDSIFTLV 60  
 SSFFTELLLC SSSDLSFFIS TACLLCSFSI FSRFSRREST FCFIWSSFL MA 112

## (2) INFORMATION ON SEQ ID NO. 55:

- (i) SEQUENCE CHARACTERISTIC:  
 (A) LENGTH: 107 amino acids  
 (B) TYPE: Protein  
 (C) STRAND: individual  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN  
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TRNLEKKKKK NLFELYFIIV YFKLCFTASS TKPLECTRYI FLGVIIMMHT NTTLLKLYFI 60  
 EMHVALRSQI DIEWRLEFQNG FYILMKVWEV YPLCLFISAL WSSWHPF 107

007237000-122700